

Semen Proteomics of COVID-19 convalescent men reveals disruption of key biological pathways relevant to male reproductive function

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Table S1 A: Clinical information of COVID-19 recovered patients

Patient ID	Age	Days after recovery	COVID Symptom	CT VALUES			Semen Parameter				
				E gene	RdRp+N gene	IC gene	Sperm concentration count(mill/ml)	Motility (%)	pH	Semen Volume	Sperm morphology (%Normal)
SCT-001	36	30	Asymptomatic	25	26.8	29	32	10	8	3	6
SCT-002	37	13	Fever, Bodyache, Loss of smell	10.7	12	17	59	65	8	2	8
SCT-003	24	24	Cough, Fever, Bodyache, Headache	31.7	33	35.7	2	2	8	3	2
SCT-004	31	64	Fever	23.4	23	34.6	32	5	8	1	1
SCT-005	41	23	Asymptomatic	20.4	21.98	30.99	54	50	8	1	8
SCT-006	29	71	Asymptomatic	32	35	28.9	42	35	8	2	12
SCT-009	39	37	Asymptomatic	25	26.99	23.8	5	10	8	2	2
SCT-010	30	20	Asymptomatic	29.5	30.7	28.4	42	25	8	1	3
SCT-018	44	22	Fever, Bodyache	21.4	21.1	28.8	8	2	8	1	3
SCT-019	40	15	Asymptomatic	22.6	23.2	27.6	72	65	8	1.5	7
SCT-020	41	30	Asymptomatic	20.4	20.97	29.7	1	1	8.5	3	NA
SCT-011	36	45	Asymptomatic	25.4	27	24	24	15	8	3	7
SCT-012	41	25	Cough, Fever, Bodyache, Loss of taste & smell	13	31	25	25	30	8	3	4
SCT-013	39	35	Asymptomatic	25	27.5	29	24	30	8	2.5	3
SCT-014	42	27	Cough, Fever, Diarrhoea	28	28.98	29.2	26	10	8	1	2
SCT-015	40	16	Asymptomatic	24.6	25.4	29.9	6	2	8	2	1
SCT-016	36	21	Cough, Fever	28.7	29.1	24.8	8	10	8	0.5	2

SCT-021	36	20	Fever	24.5	25.553	29.96	12	2	8	1.5	1
SCT-022	39	58	Fever, Bodyache	12	17	15.6	1	1	8	2	NA
SCT-023	27	34	Cough, Fever, Bodyache	15	15.66	27.29	8	15	8	1.5	2

Table S1 B: Clinical information of healthy individuals

Patient ID	Age	BMI	Sperm concentration count(mill/ml)	Motility (%)	pH	Semen Volume	Sperm morphology (%Normal)	Abstinence
Control 1	34	25	55	75	8	5	10	3
Control 2	42	26.6	28	40	8	1.5	4	>3
Control 3	37	24.5	56	60	8	2	7	>3
Control 4	35	26.7	78	45	8	1	15	3
Control 5	32	20.2	53	45	8	1.5	9	>3
Control 6	32	20.4	49	60	8	2.5	16	3
Control 7	28	22.7	36	55	8	1.5	14	3
Control 8	40	26.7	30	80	8	2	6	>3
Control 9	33	24.5	17	40	8	2.5	4	2
Control 10	40	36.3	36	45	8	4	8	>3

Table S2: Demographic representation of semen parameters in all individuals

Group (n)	Control (n=10)	Recovered (n=20)	P value
	Median (IQR)	Median (IQR)	
Age	34.5(28-42)	38 (24-44)	
Sperm concentration count (mill/mL)	42.5 (17-78)	24 (1-72)	0.013773
Motility (%)	50(40-80)	10(0-65)	1.13074E-05
pH	8	8(8-8.5)	0.329877
Semen Volume (mL)	2(1-5)	2(0.5-3)	0.295377
Sperm morphology (%Normal)	8.5(4-16)	2.5(1-12)	0.005239

Table S3: Sample-wise correlation analysis

	C12	C13	C15	C10	C11	C7	C8	C9	C5	C6	SCT006	SCT0010	SCT009	SCT002	SCT003	SCT001	SCT004	SCT0011	SCT0012	SCT0013	SCT0014	SCT0015	SCT0016	SCT005	SCT0018	SCT0019	SCT0020
C12	1	0.85475	0.79949	0.83052	0.81093	0.84293	0.75626	0.79862	0.82496	0.86498	0.85371	0.87193	0.85289	0.79265	0.81753	0.79076	0.74602	0.80539	0.82603	0.83362	0.83215	0.81382	0.78788	0.77368	0.79322	0.81831	0.8733
C13	0.85475	1	0.74921	0.79514	0.83383	0.82781	0.76434	0.79438	0.80689	0.82208	0.79608	0.83455	0.84241	0.79703	0.82412	0.79466	0.75928	0.82176	0.84717	0.83712	0.85872	0.84889	0.77576	0.78975	0.85039	0.78735	0.8716
C15	0.79949	0.74921	1	0.77655	0.79415	0.76734	0.78933	0.75	0.73221	0.79309	0.81126	0.81803	0.78236	0.78369	0.73763	0.78808	0.74388	0.82087	0.82487	0.772	0.79352	0.75318	0.71814	0.76478	0.79613	0.83642	0.80775
C10	0.83052	0.79514	0.77655	1	0.87455	0.88397	0.81852	0.88069	0.8473	0.8556	0.84646	0.85088	0.82888	0.82881	0.79634	0.81012	0.81156	0.82315	0.8131	0.80825	0.81438	0.77876	0.7055	0.81877	0.79154	0.8527	0.8404
C11	0.81093	0.83383	0.79415	0.87455	1	0.86552	0.83823	0.85883	0.81558	0.84316	0.81671	0.85393	0.85021	0.82063	0.8145	0.82949	0.82081	0.83827	0.83479	0.82345	0.83125	0.79463	0.68935	0.83115	0.84846	0.83865	0.84841
C7	0.84293	0.82781	0.76734	0.88397	0.86552	1	0.82706	0.88085	0.84392	0.84428	0.8384	0.84079	0.82369	0.82786	0.80239	0.83921	0.79113	0.84554	0.85216	0.82445	0.83852	0.83186	0.7354	0.80043	0.79427	0.84707	0.86198
C8	0.75626	0.76434	0.78933	0.81852	0.83823	0.82706	1	0.86196	0.71634	0.76449	0.76568	0.81011	0.71742	0.78594	0.69196	0.79488	0.813	0.79773	0.76612	0.70358	0.78543	0.74762	0.66548	0.81176	0.80416	0.88567	0.73986
C9	0.79862	0.79438	0.75	0.88069	0.85883	0.88085	0.86196	1	0.84452	0.81865	0.84116	0.85624	0.77482	0.82742	0.74467	0.82441	0.8459	0.84525	0.80862	0.79067	0.84227	0.80571	0.71124	0.80394	0.77861	0.87265	0.79803
C5	0.82496	0.80689	0.73221	0.8473	0.81558	0.84392	0.71634	0.84452	1	0.84152	0.85967	0.85987	0.84354	0.83028	0.82566	0.80605	0.77754	0.83807	0.81945	0.85526	0.85244	0.80993	0.7524	0.76601	0.79475	0.81312	0.83356
C6	0.86498	0.82208	0.79309	0.8556	0.84316	0.84428	0.76449	0.81865	0.84152	1	0.84997	0.88652	0.82643	0.79363	0.81885	0.81136	0.76103	0.80667	0.80768	0.81299	0.81786	0.78203	0.74074	0.80595	0.79604	0.84109	0.86013
SCT006	0.85371	0.79608	0.81126	0.84646	0.81671	0.8384	0.76568	0.84116	0.85967	0.84997	1	0.90434	0.83612	0.82217	0.77515	0.79053	0.79948	0.83823	0.8519	0.83913	0.85706	0.83323	0.79359	0.75792	0.77932	0.87855	0.82002
SCT0010	0.87193	0.83455	0.81803	0.85088	0.85393	0.84079	0.81011	0.85624	0.85987	0.88634	0.90434	1	0.85144	0.81687	0.7988	0.82332	0.79912	0.85086	0.83107	0.82524	0.85003	0.80897	0.77552	0.8015	0.81455	0.86633	0.83603
SCT009	0.85289	0.84241	0.78236	0.82888	0.85021	0.82369	0.71742	0.77482	0.84354	0.82643	0.83612	0.85144	1	0.81444	0.84827	0.80554	0.7438	0.84018	0.85516	0.86761	0.85352	0.82639	0.76145	0.74525	0.83579	0.76386	0.89912
SCT002	0.79265	0.79703	0.78369	0.82881	0.82063	0.82786	0.78594	0.82742	0.83028	0.79363	0.82217	0.81687	0.81444	1	0.84046	0.87149	0.8331	0.85769	0.82995	0.82696	0.85211	0.81099	0.74309	0.81663	0.80954	0.79407	0.81539
SCT003	0.81753	0.82412	0.73763	0.79634	0.8145	0.80239	0.69196	0.74467	0.82566	0.81885	0.77515	0.7988	0.84827	0.84046	1	0.82698	0.78313	0.80069	0.82046	0.84123	0.81085	0.80573	0.73154	0.76649	0.81127	0.73478	0.8589

SCT0 01	0.79076	0.79466	0.78808	0.81012	0.82949	0.83921	0.79488	0.82441	0.80605	0.81136	0.79053	0.82332	0.80554	0.87149	0.82698	1	0.82283	0.88974	0.82993	0.82116	0.83716	0.80153	0.71404	0.8205	0.80322	0.79969	0.82303
SCT0 04	0.74602	0.75928	0.74388	0.81156	0.82081	0.79113	0.813	0.8459	0.77754	0.76103	0.79948	0.79912	0.7438	0.8331	0.78313	0.82283	1	0.80865	0.76585	0.75168	0.79122	0.79379	0.69442	0.78473	0.78527	0.82934	0.74654
SCT0 011	0.80539	0.82176	0.82087	0.82315	0.83827	0.84554	0.79773	0.84525	0.83807	0.80667	0.83823	0.85086	0.84018	0.85769	0.80069	0.88974	0.80865	1	0.90285	0.87767	0.91273	0.8602	0.80091	0.79685	0.83418	0.83269	0.84723
SCT0 012	0.82603	0.84717	0.82487	0.8131	0.83479	0.85216	0.76612	0.8086	0.81945	0.80768	0.8519	0.83107	0.85516	0.82995	0.82046	0.82993	0.76585	0.90285	1	0.88889	0.89947	0.87087	0.79975	0.78866	0.84013	0.8186	0.858
SCT0 013	0.83362	0.83712	0.772	0.80825	0.82345	0.82445	0.70358	0.79062	0.85526	0.81299	0.83913	0.82524	0.86761	0.82696	0.84123	0.82116	0.75168	0.87767	0.88889	1	0.91197	0.86523	0.82109	0.75836	0.81438	0.76734	0.87732
SCT0 014	0.83215	0.85872	0.79352	0.81438	0.83125	0.83852	0.78543	0.84227	0.85244	0.81786	0.85706	0.85003	0.85352	0.85211	0.81085	0.83716	0.79122	0.91273	0.89947	0.91197	1	0.89347	0.83662	0.78651	0.82203	0.81664	0.85309
SCT0 015	0.81382	0.84889	0.75318	0.77876	0.79463	0.83186	0.74762	0.80571	0.80993	0.78203	0.83323	0.80897	0.82639	0.8109	0.80573	0.80153	0.79379	0.8602	0.87087	0.86523	0.89347	1	0.86544	0.72457	0.81821	0.79142	0.82196
SCT0 016	0.78788	0.77576	0.71814	0.7055	0.68935	0.7354	0.66548	0.71124	0.7524	0.74074	0.79359	0.77552	0.76145	0.74309	0.73154	0.71404	0.69442	0.80091	0.79975	0.82109	0.83662	0.86544	1	0.65761	0.74723	0.74701	0.75817
SCT0 05	0.77368	0.78975	0.76478	0.81877	0.83115	0.80043	0.81176	0.80394	0.76601	0.80595	0.75792	0.8015	0.74525	0.81663	0.76649	0.8205	0.78473	0.79685	0.78866	0.75836	0.78651	0.72457	0.65761	1	0.79061	0.80372	0.79909
SCT0 018	0.79322	0.85039	0.79613	0.79154	0.84846	0.79427	0.80416	0.77861	0.79475	0.79604	0.77932	0.81455	0.83579	0.80954	0.8112	0.80322	0.78527	0.83418	0.84013	0.81438	0.82203	0.81821	0.74723	0.79061	1	0.80754	0.82335
SCT0 019	0.81831	0.78735	0.83642	0.8527	0.83865	0.84707	0.88567	0.87265	0.81312	0.84109	0.87855	0.86633	0.76386	0.79407	0.73477	0.79969	0.82934	0.83269	0.8186	0.76734	0.81664	0.79142	0.74701	0.80372	0.80754	1	0.7964
SCT0 020	0.8733	0.8716	0.80775	0.8404	0.84841	0.86198	0.73986	0.79803	0.83356	0.86013	0.82002	0.83603	0.89912	0.81539	0.85898	0.82303	0.74654	0.84723	0.858	0.87732	0.85309	0.82196	0.75817	0.79909	0.82335	0.7964	1

Table S4: Label free quantification datasheet

Find attached MS Excel spreadsheet

Table S5: Significant differentially expressed proteins and their fold change

Protein ID	Protein Name	FC	log2(FC)	Raw p value	-log10(p)
Q9NRW1	Ras-related protein Rab-6B	2.3013	1.2025	0.029388	1.5318
P20336	Ras-related protein Rab-3A	2.1998	1.1374	0.018716	1.7278
P62258	14-3-3 protein epsilon (14-3-3E)	1.9528	0.96555	0.00016997	3.7696
P54289	Voltage-dependent calcium channel subunit alpha-2/delta-1 (Voltage-gated calcium channel subunit alpha-2/delta-1) [Cleaved into: Voltage-dependent calcium channel subunit alpha-2-1; Voltage-dependent calcium channel subunit delta-1]	1.9096	0.93327	0.012258	1.9116
Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein) [Cleaved into: T-complex protein 1 subunit eta, N-terminally processed]	1.906	0.93054	0.00036299	3.4401
P62826	GTP-binding nuclear protein Ran (Androgen receptor-associated protein 24) (GTPase Ran) (Ras-like protein TC4) (Ras-related nuclear protein)	1.8653	0.89937	0.032796	1.4842
P00390	Glutathione reductase, mitochondrial (GR) (GRase) (EC 1.8.1.7)	1.828	0.87028	0.017889	1.7474
O43707	Alpha-actinin-4 (Non-muscle alpha-actinin 4)	1.8229	0.86624	0.0029457	2.5308
P16070	CD44 antigen (CDw44) (Epican) (Extracellular matrix receptor III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (HUTCH-I) (Heparan sulfate proteoglycan) (Hermes antigen) (Hyaluronate receptor) (Phagocytic glycoprotein 1) (PGP-1) (Phagocytic glycoprotein I) (PGP-I) (CD antigen CD44)	1.7528	0.80966	0.029986	1.5231
P14384	Carboxypeptidase M (CPM) (EC 3.4.17.12)	1.7444	0.80272	0.031962	1.4954
Q15257	Serine/threonine-protein phosphatase 2A activator (EC 5.2.1.8) (PP2A, subunit B', PR53 isoform) (Phosphotyrosyl phosphatase activator) (PTPA) (Serine/threonine-protein phosphatase 2A regulatory subunit 4) (Serine/threonine-protein phosphatase 2A regulatory subunit B')	1.7435	0.802	0.025431	1.5946
P25788	Proteasome subunit alpha type-3 (Macropain subunit C8) (Multicatalytic endopeptidase complex subunit C8) (Proteasome component C8)	1.7209	0.78318	0.012421	1.9059
P15144	Aminopeptidase N (AP-N) (hAPN) (EC 3.4.11.2) (Alanyl aminopeptidase) (Aminopeptidase M) (AP-M) (Microsomal aminopeptidase) (Myeloid plasma membrane glycoprotein CD13) (gp150) (CD antigen CD13)	1.7151	0.77828	0.0075203	2.1238
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	1.6296	0.7045	0.039741	1.4008

P13639	Elongation factor 2 (EF-2)	1.6161	0.69249	0.04364	1.3601
P07195	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46)	1.6122	0.68907	0.026084	1.5836
P31946	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	1.5869	0.66624	0.04874	1.3121
P09467	Fructose-1,6-bisphosphatase 1 (FBPase 1) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase 1) (Liver FBPase)	1.5769	0.65713	0.029101	1.5361
P27348	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	1.5699	0.65067	0.033099	1.4802
P54652	Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2)	1.5623	0.64368	0.047132	1.3267
P08238	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	1.553	0.63503	0.019927	1.7006
P45974	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.4.19.12) (Deubiquitinating enzyme 5) (Isopeptidase T) (Ubiquitin thioesterase 5) (Ubiquitin-specific-processing protease 5)	1.5508	0.63304	0.031755	1.4982
P15586	N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) (Glucosamine-6-sulfatase) (G6S)	1.5507	0.63288	0.048164	1.3173
O95716	Ras-related protein Rab-3D	1.545	0.62758	0.019476	1.7105
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (G protein subunit beta-2) (Transducin beta chain 2)	1.5289	0.61253	0.048318	1.3159
O43175	D-3-phosphoglycerate dehydrogenase (3-PGDH) (EC 1.1.1.95) (2-oxoglutarate reductase) (EC 1.1.1.399) (Malate dehydrogenase) (EC 1.1.1.37)	1.5219	0.60588	0.021197	1.6737
P02790	Hemopexin (Beta-1B-glycoprotein)	1.5152	0.59954	0.041591	1.381
Q14118	Dystroglycan (Dystrophin-associated glycoprotein 1) [Cleaved into: Alpha-dystroglycan (Alpha-DG); Beta-dystroglycan (Beta-DG)]	0.6274	-0.67255	0.0028344	2.5475
Q02818	Nucleobindin-1 (CALNUC)	0.6251	-0.67783	0.022095	1.6557
P07602	Prosaposin (Proactivator polypeptide) [Cleaved into: Saposin-A (Protein A); Saposin-B-Val; Saposin-B (Cerebroside sulfate activator) (CSAct) (Dispersin) (Sphingolipid activator protein 1) (SAP-1) (Sulfatide/GM1 activator); Saposin-C (A1 activator) (Co-beta-glucosidase) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin-D (Component C) (Protein C)]	0.62264	-0.68353	0.0055554	2.2553
Q9BRK5	45 kDa calcium-binding protein (Cab45) (Stromal cell-derived factor 4) (SDF-4)	0.61454	-0.70242	0.020379	1.6908
P04279	Semenogelin-1 (Cancer/testis antigen 103) (Semenogelin I) (SGI) [Cleaved into: Alpha-inhibin-92; Alpha-inhibin-31; Seminal basic protein]	0.60887	-0.71579	0.027814	1.5557
O76074	cGMP-specific 3',5'-cyclic phosphodiesterase (EC 3.1.4.35) (cGMP-binding cGMP-specific phosphodiesterase) (CGB-PDE)	0.60486	-0.72533	0.044579	1.3509

O00584	Ribonuclease T2 (EC 4.6.1.19) (Ribonuclease 6)	0.58843	-0.76506	5.92E-05	4.2276
Q9H3G5	Probable serine carboxypeptidase CPVL (EC 3.4.16.-) (Carboxypeptidase, vitellogenic-like) (Vitellogenic carboxypeptidase-like protein) (VCP-like protein) (hVLP)	0.58295	-0.77856	0.019274	1.715
O43291	Kunitz-type protease inhibitor 2 (Hepatocyte growth factor activator inhibitor type 2) (HAI-2) (Placental bikunin)	0.57051	-0.80967	0.016135	1.7922
Q8N114	Protein shisa-5 (Putative NF-kappa-B-activating protein 120) (Scotin)	0.56271	-0.82954	0.022796	1.6421
P02511	Alpha-crystallin B chain (Alpha(B)-crystallin) (Heat shock protein beta-5) (HspB5) (Renal carcinoma antigen NY-REN-27) (Rosenthal fiber component)	0.54575	-0.87368	0.00098959	3.0045
O60568	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 [Includes: Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 (EC 1.14.11.4) (Lysyl hydroxylase 3) (LH3); Procollagen glycosyltransferase (EC 2.4.1.50) (EC 2.4.1.66) (Galactosylhydroxylysine-glucosyltransferase) (Procollagen galactosyltransferase) (Procollagen glucosyltransferase)]	0.54043	-0.88781	0.0075455	2.1223
O14786	Neuropilin-1 (Vascular endothelial cell growth factor 165 receptor) (CD antigen CD304)	0.50342	-0.99016	0.015979	1.7964
Q92743	Serine protease HTRA1 (EC 3.4.21.-) (High-temperature requirement A serine peptidase 1) (L56) (Serine protease 11)	0.50239	-0.99311	0.0085106	2.07
P02743	Serum amyloid P-component (SAP) (9.5S alpha-1-glycoprotein) [Cleaved into: Serum amyloid P-component(1-203)]	0.49931	-1.002	0.0055571	2.2552
P28799	Progranulin (PGRN) (Acrogranin) (Epithelin precursor) (Glycoprotein of 88 Kda) (GP88) (Glycoprotein 88) (Granulin precursor) (PC cell-derived growth factor) (PCDGF) (Proepithelin) (PEPI) [Cleaved into: Paragranulin; Granulin-1 (Granulin G); Granulin-2 (Granulin F); Granulin-3 (Epithelin-2) (Granulin B); Granulin-4 (Epithelin-1) (Granulin A); Granulin-5 (Granulin C); Granulin-6 (Granulin D); Granulin-7 (Granulin E)]	0.48333	-1.0489	0.0027169	2.5659
P13987	CD59 glycoprotein (1F5 antigen) (20 kDa homologous restriction factor) (HRF-20) (HRF20) (MAC-inhibitory protein) (MAC-IP) (MEM43 antigen) (Membrane attack complex inhibition factor) (MACIF) (Membrane inhibitor of reactive lysis) (MIRL) (Protectin) (CD antigen CD59)	0.46818	-1.0949	0.00013139	3.8814
P98095	Fibulin-2 (FIBL-2)	0.38565	-1.3746	0.038169	1.4183
P24593	Insulin-like growth factor-binding protein 5 (IBP-5) (IGF-binding protein 5) (IGFBP-5)	0.31875	-1.6495	0.02328	1.633
Q9BUN1	Protein MENT (Methylated in normal thymocytes protein)	0.26787	-1.9004	0.0089832	2.0466
Q9H4B8	Dipeptidase 3 (EC 3.4.13.19)	0.22145	-2.175	0.024391	1.6128

Table S6: Functional annotation of proteins dysregulated in COVID-19 recovered group

Molecular function	Proteins	Percentage
Binding (GO:0005488)	45	39.1
Catalytic activity (GO:0003824)	57	49.6
Molecular adaptor activity (GO:0060090)	1	0.9
Molecular function regulator (GO:0098772)	6	5.2
Molecular transducer activity (GO:0060089)	2	1.7
Translation regulator activity (GO:0045182)	2	1.7
Transporter activity (GO:0005215)	2	1.7
Cellular Components	Proteins	Percentage
Cellular anatomical entity (GO:0110165)	87	52.1
Intracellular (GO:0005622)	58	34.7
Protein-containing complex (GO:0032991)	22	13.2

Table S7: Pathways upregulated and downregulated in COVID-19 recovered group

Upregulated pathway						
Group ID	Description	LogP	Log(q-value)	InTerm_InList	Genes	Symbols
1_Summary	regulated exocytosis	-11.26063	-6.924	18/780	81,290,335,823,960,961,1938,2799,3240,3326,3827,5864,7879,8655,9545,9948,10576,6414,4192	ACTN4,ANPEP,APOA1,CAPN1,CD44,CD47,EEF2,GNS,HP,HSP90AB1,KNG1,RAB3A,RAB7A,DYNLL1,RAB3D,WDR1,CCT2,TMBIM1,MDK
2_Summary	Vesicle-mediated transport	-8.20851	-4.996	14/673	60,335,830,2664,2799,3240,3263,5864,7529,7531,7879,8655,10971,51560,9368,9545,50848,64114	ACTB,APOA1,CAPZA2,GDI1,GNS,HP,HPX,RAB3A,YWHAB,YWHAE,RAB7A,DYNLL1,YWHAQ,RAB6B,SLC9A3R1,RAB3D,F11R,TMBIM1
3_Summary	positive regulation of establishment of protein localization	-7.452703	-4.270	10/331	3326,5566,5901,7529,7531,8655,9520,10574,10576,10971,60,2664,64114,3306,5682,5684,10856,23345,7879,5864,9545,81,9368,506,4830,4192	HSP90AB1,PRKACA,RAN,YWHAB,YWHAE,DYNLL1,NPEPPS,CCT7,CCT2,YWHAQ,ACTB,GDI1,TMBIM1,HSPA2,PSMA1,PSMA3,RUVBL2,SYNE1,RAB7A,RAB3A,RAB3D,ACTN4,SLC9A3R1,ATP5F1B,NME1,MDK
4_Summary	Kinase maturation complex 1	-6.968671	-3.840	4/16	3326,7529,7531,10971,5566,5901,8655,335,961,9520,9948,10574,10576,10856,960,3306,60,2783,5682,5684,2664,64114,81,9368,1938,1311,1942,2936,50848,5524,506,7879,3240,3827,5864	HSP90AB1,YWHAB,YWHAE,YWHAQ,PRKACA,RAN,DYNLL1,APOA1,CD47,NPEPPS,WDR1,CCT7,CCT2,RUVBL2,CD44,HSPA2,ACTB,GNB2,PSMA1,PSMA3,GDI1,TMBIM1,ACTN4,SLC9A3R1,EEF2,COMP,EFNA1,GSR,F11R,PTPA,ATP5F1B,RAB7A,HP,KNG1,RAB3A
5_Summary	HSP90 chaperone cycle for steroid hormone receptors (SHR)	-6.292649	-3.212	5/55	830,2288,3306,3326,8655,2783,10574,10576,10856,2936,4499,5682,5684,7531,5566,1311,2673	CAPZA2,FKBP4,HSPA2,HSP90AB1,DYNLL1,GNB2,CCT7,CCT2,RUVBL2,GSR,MT1M,PSMA1,PSMA3,YWHAQ,PRKACA,COMP,GFPT1

6_Summary	response to wounding	-6.175101	-3.177	12/701	60,335,780,830,960,1311,3827,4192,5566,5864,50848,199731,4830,7879	ACTB,APOA1,DDR1,CAPZA2,CD44,COMP,KNG1,MDK,PRKACA,RAB3A,F11R,CADM4,NME1,RAB7A
7_Summary	Regulation Of Transmembrane Transporter Activity	-6.009127	-3.051	8/268	60,81,781,823,3306,5566,7531,9368,335,5864,9948,10971,506,3263,3827,4499,7879,79689,290,1311,50848,51752,6565	ACTB,ACTN4,CACNA2D1,CAPN1,HSPA2,PRKACA,YWHAE,SLC9A3R1,APOA1,RAB3A,WDR1,YWHAQ,ATP5F1B,HPX,KNG1,MT1M,RAB7A,STEAP4,ANPEP,COMP,F11R,ERAP1,SLC15A2
8_Summary	Glutathione Metabolism	-5.994904	-3.051	5/63	290,2936,2944,2952,26227,3240,4499,84817,60,1938,2799,8702,50859,3326,2203,3263,10135,335,5524,4830,2783,3827,5566	ANPEP,GSR,GSTM1,GSTT1,PHGDH,HP,MT1M,TXNDC17,ACTB,EEF2,GNS,B4GALT4,SPOCK3,HSP90AB1,FBP1,HPX,NAMPT,APOA1,PTPA,NME1,GNB2,KNG1,PRKACA
9_Summary	Hemostasis	-5.841105	-2.921	11/620	60,81,335,830,960,961,2783,3827,5566,9948,50848,781,4082,4192,9368,780,823,1311,50859,1942,2288,2664,3306,7879,3326,10135,26007	ACTB,ACTN4,APOA1,CAPZA2,CD44,CD47,GNB2,KNG1,PRKACA,WDR1,F11R,CACNA2D1,MARCKS,MDK,SLC9A3R1,DDR1,CAPN1,COMP,SPOCK3,EFNA1,FKBP4,GDI1,HSPA2,RAB7A,HSP90AB1,NAMPT,TKFC
10_Summary	Folding Of Actin By CCT/Tric	-5.581854	-2.767	3/10	60,10574,10576,10856,173,335,1942,3326,5901,7531,23345,2783,9545	ACTB,CCT7,CCT2,RUVBL2,AFM,APOA1,EFNA1,HSP90AB1,RAN,YWHAE,SYNE1,GNB2,RAB3D
11_Summary	P2X7 Receptor Signalling Complex	-5.320397	-2.564	3/12	60,81,3326,961,8655,311,335,7879,26227,3240,5864	ACTB,ACTN4,HSP90AB1,CD47,DYNLL1,ANXA11,APOA1,RAB7A,PHGDH,HP,RAB3A
12_Summary	Scavenging Of Heme From Plasma	-5.207345	-2.502	3/13	335,3240,3263,4499,79689	APOA1,HP,HPX,MT1M,STEAP4
13_Summary	Regulation Of Cell Morphogenesis	-5.001795	-2.375	9/486	81,335,960,1942,2664,4192,9368,9948,50848,506,780,961,3827,2783,4830,5682,26007	ACTN4,APOA1,CD44,EFNA1,GDI1,MDK,SLC9A3R1,WDR1,F11R,ATP5F1B,DDR1,CD47,KNG1,GNB2,NME1,PSMA1,TKFC

14_Summary	Antigen Processing And Presentation Of Peptide Antigen	-4.708336	-2.181	6/194	830,5682,5684,7879,8655,51752,5566,7529,9520,51560,2673,5238,8702	CAPZA2,PSMA1,PSMA3,RAB7A,DYNLL1,ERAP1,PRKACA,YWHAB,NPEPPS,RAB6B,GFPT1,PGM3,B4GALT4
15_Summary	Morphogenesis Of An Epithelium	-4.665561	-2.170	9/536	60,780,960,4192,5566,5682,5684,9368,9948,3263,3326,6565,26007,51752,961,81,335,84817,10856,8078,9097,1942,7879,7529,3827,5864,5901,8655,2783	ACTB,DDR1,CD44,MDK,PRKACA,PSMA1,PSMA3,SLC9A3R1,WDR1,HPX,HSP90AB1,SLC15A2,TKFC,ERAP1,CD47,ACTN4,APOA1,TXNDC17,RUVBL2,USP5,USP14,EFNA1,RAB7A,YWHAB,KNG1,RAB3A,RAN,DYNLL1,GNB2
16_Summary	Cell Morphogenesis Involved In Differentiation	-4.415086	-2.008	10/723	60,81,335,1942,2664,3326,4192,5864,9368,9948,3306,5524,8655,50848,780,960,2288,4830,5566	ACTB,ACTN4,APOA1,EFNA1,GDI1,HSP90AB1,MDK,RAB3A,SLC9A3R1,WDR1,HSPA2,PTPA,DYNLL1,F11R,DDR1,CD44,FKBP4,NME1,PRKACA
17_Summary	Negative Regulation Of Hydrolase Activity	-4.309572	-1.942	8/459	335,960,3827,5524,7531,9097,50848,50859,1942,3326,5684	APOA1,CD44,KNG1,PTPA,YWHA,USP14,F11R,SPOCK3,EFNA1,HSP90AB1,PSMA3
18_Summary	Negative Regulation Of Phosphate Metabolic Process	-4.279424	-1.931	9/601	1942,2203,5524,7529,7531,8000,8655,9368,199731,60,780,7879,10135,960,26007	EFNA1,FBP1,PTPA,YWHAB,YWHA,EFNA1,PSCA,DYNLL1,SLC9A3R1,CADM4,ACTB,DDR1,RAB7A,NAMPT,CD44,TKFC
19_Summary	Peptide Catabolic Process	-4.027014	-1.754	3/31	290,9520,51752	ANPEP,NPEPPS,ERAP1
20_Summary	Tight Junction	-3.897463	-1.685	5/170	60,81,5566,9368,50848,961,781,7879	ACTB,ACTN4,PRKACA,SLC9A3R1,F11R,CD47,CACNA2D1,RAB7A

Downregulated pathways						
Group ID	Description	LogP	Log(q-value)	InTerm_InList	Genes	Symbols
1_Summary	Regulated Exocytosis	-16.69693	-12.338	22/780	387,966,2896,4069,5236,5660,5686,5718,6515,7040,7057,70	RHOA,CD59,GRN,LYZ,PGM1,PSAP,PSMA5,PSMD12,SLC2A3,TGFB1,T

					94,8407,8635,9066,10043,10493,10890,23385,29789,51150,55276,8754	HBS1,TLN1,TAGLN2,RNASET2,SYT7,TOM1,VAT1,RAB10,NCSTN,OLA1,SDF4,PGM2,ADAM9
2_Summary	Morphogenesis Of An Epithelium	-7.958054	-4.745	12/536	387,1605,3488,5686,5711,5718,7040,8829,8985,9491,10653,10890,8607,7094,10096,23385,2629,7057,4507,5184,7407,8754,8815,10434,4957,1410,325,5236,8635,8654,966,2896	RHOA,DAG1,IGFBP5,PSMA5,PSMD5,PSMD12,TGFB1,NRP1,PLOD3,PSMF1,SPINT2,RAB10,RUVBL1,TLN1,ACTR3,NCSTN,GBA,THBS1,MTAP,PEPD,VAR1,ADAM9,BANF1,LYPLA1,ODF2,CRYAB,APCS,PGM1,RNASET2,PDE5A,CD59,GRN
3_Summary	Carbohydrate Derivative Catabolic Process	-7.337504	-4.155	8/200	2629,3423,3425,4507,6448,7040,8654,55276,5236,11041,5634,54187,6515,29789	GBA,IDS,IDUA,MTAP,SGSH,TGFB1,PDE5A,PGM2,PGM1,B4GAT1,PRPS2,NANS,SLC2A3,OLA1
4_Summary	Negative Regulation Of Cellular Component Movement	-6.280703	-3.201	9/378	387,1605,3488,5176,6406,7040,7057,8829,10653,2896,8754,5654,23385,7094,2629,4507,8815,2199,10096,1410,10434,10493,5660,8985,6697,10890	RHOA,DAG1,IGFBP5,SERPINF1,SEMG1,TGFB1,THBS1,NRP1,SPINT2,GRN,ADAM9,HTRA1,NCSTN,TLN1,GBA,MTAP,BANF1,FBLN2,ACTR3,CRYAB,LYPLA1,VAT1,PSAP,PLOD3,SPR,RAB10
5_Summary	Platelet Degranulation	-6.016252	-2.988	6/128	5660,7040,7057,7094,8407,29789,387,8654	PSAP,TGFB1,THBS1,TLN1,TAGLN2,OLA1,RHOA,PDE5A
6_Summary	Extracellular Matrix Organization	-5.985303	-2.988	8/301	1605,2199,5654,7040,7057,8754,8985,23385,10653,5184,307,5176,113791	DAG1,FBLN2,HTRA1,TGFB1,THBS1,ADAM9,PLOD3,NCSTN,SPINT2,PEPD,ANXA4,SERPINF1,PIK3IP1
7_Summary	Heparan Sulfate Degradation	-5.874431	-2.932	3/9	3423,3425,6448,1605,5236,7057,11041,5634,55276,2629,5660,7040,325,8985,23385	IDS,IDUA,SGSH,DAG1,PGM1,THBS1,B4GAT1,PRPS2,PGM2,GBA,PSAP,TGFB1,APCS,PLOD3,NCSTN
8_Summary	Post-Translational Protein Modification	-5.390978	-2.612	8/362	3488,4924,5686,5711,5718,8404,9491,51246,2199,7057,375616	IGFBP5,NUCB1,PSMA5,PSMD5,PSMD12,SPARCL1,PSMF1,SHISA5,FBLN2,THBS1,KCP
9_Summary	Response To Wounding	-4.93801	-2.371	10/701	325,387,966,1605,2896,7040,7057,7094,8829,9066,5654	APCS,RHOA,CD59,DAG1,GRN,TGFB1,THBS1,TLN1,NRP1,SYT7,HTRA1

10_Summary	Membrane Protein Proteolysis	-4.734535	-2.310	4/61	1605,7040,8754,23385,2629,2896,51150,6406,5654	DAG1,TGFB1,ADAM9,NCSTN,GBA,GRN,SDF4,SEMG1,HTRA1
11_Summary	Regulation Of Peptidase Activity	-4.651158	-2.256	8/458	1410,2896,5176,6406,7057,9491,10653,23385,48,8754,9066,966,325	CRYAB,GRN,SERPINF1,SEMG1,THBS1,PSMF1,SPINT2,NCSTN,ACO1,ADAM9,SYT7,CD59,APCS
12_Summary	Negative Regulation Of Response To External Stimulus	-4.262183	-2.024	7/381	325,2629,2896,5176,5654,7057,8829,9066,1410,1605,3488,4924,8754	APCS,GBA,GRN,SERPINF1,HTRA1,THBS1,NRP1,SYT7,CRYAB,DAG1,IGFBP5,NUCB1,ADAM9
13_Summary	Basement Membrane Organization	-4.206952	-2.000	3/30	1605,8985,10653,2199,8829,325,3488	DAG1,PLOD3,SPINT2,FBLN2,NRP1,APCS,IGFBP5
14_Summary	Response To Testosterone	-3.796491	-1.714	3/41	2629,4507,7057,5634	GBA,MTAP,THBS1,PRPS2
15_Summary	Epithelial Cell Differentiation	-3.777782	-1.698	9/781	307,387,5660,8407,8754,8829,8985,10653,10890	ANXA4,RHOA,PSAP,TAGLN2,ADAM9,NRP1,PLOD3,SPINT2,RAB10
16_Summary	Amyloid Fiber Formation	-3.731687	-1.665	4/110	325,4069,6406,23385,1605,387,2629	APCS,LYZ,SEMG1,NCSTN,DAG1,RHOA,GBA
17_Summary	Diseases Of Glycosylation	-3.297904	-1.364	4/143	1605,5236,7057,11041	DAG1,PGM1,THBS1,B4GAT1
18_Summary	Sperm-Egg Recognition	-3.283987	-1.353	3/61	11055,53340,246777	ZPBP,SPA17,SPESP1
19_Summary	Carbohydrate Derivative Biosynthetic Process	-3.06317	-1.181	8/783	4507,5236,5634,7040,8985,11041,23385,54187,2629	MTAP,PGM1,PRPS2,TGFB1,PLOD3,B4GAT1,NCSTN,NANS,GBA
20_Summary	Ephrin Receptor Signaling Pathway	-2.84998	-1.011	3/86	387,10096,23385,10653,10890,3488,7040,7057,8829	RHOA,ACTR3,NCSTN,SPINT2,RAB10,IGFBP5,TGFB1,THBS1,NRP1

Table S8: SRM peptide and transition list

Protein Name	Peptide Modified Sequence	Precursor Mz	Precursor Charge	Collision Energy	Product Mz	Product Charge	Fragment Ion	Fragment Ion Type	Fragment Ion Ordinal	Cleavage Aa
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	1075.531955	1	y9	y	9	F
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	928.463541	1	y8	y	8	S
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	841.431512	1	y7	y	7	Q
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	713.372935	1	y6	y	6	F
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	566.304521	1	y5	y	5	P
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	469.251757	1	y4	y	4	H
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	332.192845	1	y3	y	3	G
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	694.833308	2	y12	y	12	P
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	751.37534	2	0	538.269615	2	y9	y	9	F
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	505.236501	1	y4	y	4	D
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	390.209558	1	y3	y	3	Q
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	779.337474	2	y13	y	13	T
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	728.813635	2	y12	y	12	Y
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	647.281971	2	y11	y	11	H
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	578.752515	2	y10	y	10	V
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	471.704837	2	y8	y	8	A
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	436.18628	2	y7	y	7	N
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	379.164816	2	y6	y	6	D
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	1170.517427	2	0	321.651344	2	y5	y	5	H
sp P04279 SEMG1_HUMAN	HLGGSQQLLHNK	666.362567	2	0	967.531955	1	y8	y	8	S
sp P04279 SEMG1_HUMAN	HLGGSQQLLHNK	666.362567	2	0	880.499926	1	y7	y	7	Q

sp P04279 SEMG1_HUMAN	HLGGSQQLLHNK	666.362567	2	0	752.441349	1	y6	y	6	Q
sp P04279 SEMG1_HUMAN	HLGGSQQLLHNK	666.362567	2	0	624.382771	1	y5	y	5	L
sp P04279 SEMG1_HUMAN	HLGGSQQLLHNK	666.362567	2	0	511.298707	1	y4	y	4	L
sp P04279 SEMG1_HUMAN	HLGGSQQLLHNK	666.362567	2	0	398.214643	1	y3	y	3	H
sp P04279 SEMG1_HUMAN	HLGGSQQLLHNK	666.362567	2	0	484.269615	2	y8	y	8	S
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	1026.448679	1	y8	y	8	Q
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	898.390101	1	y7	y	7	Y
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	735.326772	1	y6	y	6	S
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	648.294744	1	y5	y	5	N
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	534.251817	1	y4	y	4	T
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	433.204138	1	y3	y	3	E
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	513.727977	2	y8	y	8	Q
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	685.81277	2	0	368.167024	2	y6	y	6	S
sp P04279 SEMG1_HUMAN	EQTSVSGAQK	517.759277	2	0	589.330401	1	y6	y	6	V
sp P04279 SEMG1_HUMAN	EQTSVSGAQK	517.759277	2	0	490.261987	1	y5	y	5	S
sp P04279 SEMG1_HUMAN	EQTSVSGAQK	517.759277	2	0	403.229959	1	y4	y	4	G
sp P04279 SEMG1_HUMAN	EQTSVSGAQK	517.759277	2	0	346.208495	1	y3	y	3	A
sp P04279 SEMG1_HUMAN	EQTSVSGAQK	517.759277	2	0	295.168839	2	y6	y	6	V
sp P04279 SEMG1_HUMAN	EQTSVSGAQK	517.759277	2	0	202.118617	2	y4	y	4	G
sp P04279 SEMG1_HUMAN	QGGSQSSYVLQTEELVANK	1019.508008	2	0	1493.7846	1	y13	y	13	S
sp P04279 SEMG1_HUMAN	QGGSQSSYVLQTEELVANK	1019.508008	2	0	1406.752572	1	y12	y	12	Y
sp P04279 SEMG1_HUMAN	QGGSQSSYVLQTEELVANK	1019.508008	2	0	1243.689243	1	y11	y	11	V
sp P04279 SEMG1_HUMAN	QGGSQSSYVLQTEELVANK	1019.508008	2	0	1144.620829	1	y10	y	10	L
sp P04279 SEMG1_HUMAN	QGGSQSSYVLQTEELVANK	1019.508008	2	0	1031.536765	1	y9	y	9	Q
sp P04279 SEMG1_HUMAN	QGGSQSSYVLQTEELVANK	1019.508008	2	0	903.478188	1	y8	y	8	T
sp P04279 SEMG1_HUMAN	QGGSQSSYVLQTEELVANK	1019.508008	2	0	802.430509	1	y7	y	7	E

sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	673.387916	1	y6	y	6	E
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	544.345323	1	y5	y	5	L
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	431.261259	1	y4	y	4	V
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	332.192845	1	y3	y	3	A
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	854.941241	2	y15	y	15	Q
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	747.395938	2	y13	y	13	S
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	572.814053	2	y10	y	10	L
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	516.272021	2	y9	y	9	Q
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	452.242732	2	y8	y	8	T
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	401.718893	2	y7	y	7	E
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	337.197596	2	y6	y	6	E
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	1019.508008	2	0	216.134267	2	y4	y	4	V
sp P04279 SEMG1_HUMAN	GHYQNVVEVR	600.809636	2	0	715.409714	1	y6	y	6	N
sp P04279 SEMG1_HUMAN	GHYQNVVEVR	600.809636	2	0	502.298373	1	y4	y	4	V
sp P04279 SEMG1_HUMAN	GHYQNVVEVR	600.809636	2	0	403.229959	1	y3	y	3	E
sp P04279 SEMG1_HUMAN	GHYQNVVEVR	600.809636	2	0	358.208495	2	y6	y	6	N
sp P04279 SEMG1_HUMAN	GHYQNVVEVR	600.809636	2	0	301.187031	2	y5	y	5	V
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	968.461826	1	y8	y	8	L
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	855.377762	1	y7	y	7	C
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	695.347114	1	y6	y	6	P
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	598.29435	1	y5	y	5	A
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	527.257236	1	y4	y	4	H
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	390.198324	1	y3	y	3	Q
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	484.734551	2	y8	y	8	L
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	428.192519	2	y7	y	7	C
sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	348.177195	2	y6	y	6	P

sp P04279 SEMG1_HUMAN	VQTSLC[+57]PAHQDK	692.3379	2	0	264.132256	2	y4	y	4	H
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	1222.631394	1	y10	y	10	T
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	1121.583716	1	y9	y	9	Q
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	993.525138	1	y8	y	8	D
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	878.498195	1	y7	y	7	E
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	749.455602	1	y6	y	6	L
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	636.371538	1	y5	y	5	L
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	523.287474	1	y4	y	4	V
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	424.21906	1	y3	y	3	Y
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	611.819335	2	y10	y	10	T
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	561.295496	2	y9	y	9	Q
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	842.92506	2	0	497.266207	2	y8	y	8	D
sp P04279 SEMG1_HUMAN	NLNQDQQHGR	605.289599	2	0	740.343426	1	y6	y	6	D
sp P04279 SEMG1_HUMAN	NLNQDQQHGR	605.289599	2	0	625.316482	1	y5	y	5	Q
sp P04279 SEMG1_HUMAN	NLNQDQQHGR	605.289599	2	0	497.257905	1	y4	y	4	Q
sp P04279 SEMG1_HUMAN	NLNQDQQHGR	605.289599	2	0	369.199327	1	y3	y	3	H
sp P04279 SEMG1_HUMAN	NLNQDQQHGR	605.289599	2	0	370.675351	2	y6	y	6	D
sp P04279 SEMG1_HUMAN	NLNQDQQHGR	605.289599	2	0	249.13259	2	y4	y	4	Q
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	1197.549455	1	y10	y	10	P
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	1100.496691	1	y9	y	9	S
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	1013.464663	1	y8	y	8	Q
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	885.406085	1	y7	y	7	E
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	756.363492	1	y6	y	6	Q
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	628.304915	1	y5	y	5	E
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	499.262322	1	y4	y	4	H
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	362.20341	1	y3	y	3	S

sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	599.278366	2	y10	y	10	P
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	550.751984	2	y9	y	9	S
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	507.235969	2	y8	y	8	Q
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	826.915558	2	0	443.206681	2	y7	y	7	E
sp P04279 SEMG1_HUMAN	SQIQAPNPK	491.769448	2	0	526.298373	1	y5	y	5	A
sp P04279 SEMG1_HUMAN	SQIQAPNPK	491.769448	2	0	455.261259	1	y4	y	4	P
sp P04279 SEMG1_HUMAN	SQIQAPNPK	491.769448	2	0	358.208495	1	y3	y	3	N
sp P04279 SEMG1_HUMAN	SQIQAPNPK	491.769448	2	0	263.652824	2	y5	y	5	A
sp P04279 SEMG1_HUMAN	SQIQAPNPK	491.769448	2	0	228.134267	2	y4	y	4	P
sp P04279 SEMG1_HUMAN	SQIQAPNPK	491.769448	2	0	179.607886	2	y3	y	3	N
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	938.447891	1	y8	y	8	P
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	655.315814	1	y6	y	6	H
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	518.256902	1	y5	y	5	G
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	461.235438	1	y4	y	4	E
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	332.192845	1	y3	y	3	N
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	469.727583	2	y8	y	8	P
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	328.161545	2	y6	y	6	H
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	231.121357	2	y4	y	4	E
sp P04279 SEMG1_HUMAN	QEPWHGENAK	598.278169	2	0	166.600061	2	y3	y	3	N
sp P04279 SEMG1_HUMAN	EQDLSHEQK	613.804216	2	0	741.388979	1	y6	y	6	L
sp P04279 SEMG1_HUMAN	EQDLSHEQK	613.804216	2	0	628.304915	1	y5	y	5	S
sp P04279 SEMG1_HUMAN	EQDLSHEQK	613.804216	2	0	541.272886	1	y4	y	4	H
sp P04279 SEMG1_HUMAN	EQDLSHEQK	613.804216	2	0	404.213974	1	y3	y	3	E
sp P04279 SEMG1_HUMAN	EQDLSHEQK	613.804216	2	0	371.198127	2	y6	y	6	L
sp P04279 SEMG1_HUMAN	EQDLSHEQK	613.804216	2	0	314.656095	2	y5	y	5	S
sp P04279 SEMG1_HUMAN	EQDLSHEQK	613.804216	2	0	271.140081	2	y4	y	4	H

sp Q9BS86 ZPBP1_HUMAN	VPSSVGHLVR	525.806365	2	0	581.351805	1	y5	y	5	G
sp Q9BS86 ZPBP1_HUMAN	VPSSVGHLVR	525.806365	2	0	524.330342	1	y4	y	4	H
sp Q9BS86 ZPBP1_HUMAN	VPSSVGHLVR	525.806365	2	0	387.27143	1	y3	y	3	L
sp Q9BS86 ZPBP1_HUMAN	VPSSVGHLVR	525.806365	2	0	340.713748	2	y6	y	6	V
sp Q9BS86 ZPBP1_HUMAN	VPSSVGHLVR	525.806365	2	0	194.139353	2	y3	y	3	L
sp Q9BS86 ZPBP1_HUMAN	IVGSTSFPVK	517.797674	2	0	678.382102	1	y6	y	6	T
sp Q9BS86 ZPBP1_HUMAN	IVGSTSFPVK	517.797674	2	0	490.302396	1	y4	y	4	F
sp Q9BS86 ZPBP1_HUMAN	IVGSTSFPVK	517.797674	2	0	343.233982	1	y3	y	3	P
sp Q9BS86 ZPBP1_HUMAN	IVGSTSFPVK	517.797674	2	0	339.694689	2	y6	y	6	T
sp Q9BS86 ZPBP1_HUMAN	IVGSTSFPVK	517.797674	2	0	289.17085	2	y5	y	5	S
sp Q9BS86 ZPBP1_HUMAN	IVGSTSFPVK	517.797674	2	0	245.654836	2	y4	y	4	F
sp Q9BS86 ZPBP1_HUMAN	IVGSTSFPVK	517.797674	2	0	172.120629	2	y3	y	3	P
sp Q9BS86 ZPBP1_HUMAN	SPHVLC[+57]VTQQLR	719.385185	2	0	904.466912	1	y7	y	7	C
sp Q9BS86 ZPBP1_HUMAN	SPHVLC[+57]VTQQLR	719.385185	2	0	744.436263	1	y6	y	6	V
sp Q9BS86 ZPBP1_HUMAN	SPHVLC[+57]VTQQLR	719.385185	2	0	645.367849	1	y5	y	5	T
sp Q9BS86 ZPBP1_HUMAN	SPHVLC[+57]VTQQLR	719.385185	2	0	544.320171	1	y4	y	4	Q
sp Q9BS86 ZPBP1_HUMAN	SPHVLC[+57]VTQQLR	719.385185	2	0	416.261593	1	y3	y	3	Q
sp Q9BS86 ZPBP1_HUMAN	SPHVLC[+57]VTQQLR	719.385185	2	0	675.869171	2	y11	y	11	P
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	1337.652464	1	y11	y	11	I
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	1012.488693	1	y8	y	8	S
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	925.456664	1	y7	y	7	F
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	778.38825	1	y6	y	6	Q
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	650.329673	1	y5	y	5	W
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	464.25036	1	y4	y	4	Y
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	669.32987	2	y11	y	11	I
sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	506.747984	2	y8	y	8	S

sp Q9BS86 ZPBP1_HUMAN	NAELIDPSFQWYGPK	882.933219	2	0	151.097154	2	y3	y	3	G
sp Q9BS86 ZPBP1_HUMAN	LLLDLSC[+57]EISLLK	758.936385	2	0	949.502294	1	y8	y	8	S
sp Q9BS86 ZPBP1_HUMAN	LLLDLSC[+57]EISLLK	758.936385	2	0	862.470266	1	y7	y	7	C
sp Q9BS86 ZPBP1_HUMAN	LLLDLSC[+57]EISLLK	758.936385	2	0	573.397024	1	y5	y	5	I
sp Q9BS86 ZPBP1_HUMAN	LLLDLSC[+57]EISLLK	758.936385	2	0	460.31296	1	y4	y	4	S
sp Q9BS86 ZPBP1_HUMAN	LLLDLSC[+57]EISLLK	758.936385	2	0	373.280932	1	y3	y	3	L
sp Q9BS86 ZPBP1_HUMAN	LLLDLSC[+57]EISLLK	758.936385	2	0	187.144104	2	y3	y	3	L
sp Q9BS86 ZPBP1_HUMAN	C[+57]TDHNC[+57]EPYK	662.258262	2	0	696.302138	1	y5	y	5	C
sp Q9BS86 ZPBP1_HUMAN	C[+57]TDHNC[+57]EPYK	662.258262	2	0	536.271489	1	y4	y	4	E
sp Q9BS86 ZPBP1_HUMAN	C[+57]TDHNC[+57]EPYK	662.258262	2	0	407.228896	1	y3	y	3	P
sp Q9BS86 ZPBP1_HUMAN	C[+57]TDHNC[+57]EPYK	662.258262	2	0	405.676171	2	y6	y	6	N
sp Q9BS86 ZPBP1_HUMAN	C[+57]TDHNC[+57]EPYK	662.258262	2	0	348.654707	2	y5	y	5	C
sp Q9BS86 ZPBP1_HUMAN	C[+57]TDHNC[+57]EPYK	662.258262	2	0	204.118086	2	y3	y	3	P
sp Q5BJF6 ODFP2_HUMAN	SSARPVGC[+57]K	481.247826	2	0	560.286094	1	y5	y	5	P
sp Q5BJF6 ODFP2_HUMAN	SSARPVGC[+57]K	481.247826	2	0	463.23333	1	y4	y	4	V
sp Q5BJF6 ODFP2_HUMAN	SSARPVGC[+57]K	481.247826	2	0	364.164916	1	y3	y	3	G
sp Q5BJF6 ODFP2_HUMAN	SSARPVGC[+57]K	481.247826	2	0	280.646685	2	y5	y	5	P
sp Q5BJF6 ODFP2_HUMAN	SSARPVGC[+57]K	481.247826	2	0	232.120303	2	y4	y	4	V
sp Q5BJF6 ODFP2_HUMAN	SSARPVGC[+57]K	481.247826	2	0	182.586096	2	y3	y	3	G
sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	1494.725705	1	y13	y	13	P
sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	547.272218	1	y5	y	5	P
sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	796.392873	2	y14	y	14	P
sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	550.795329	2	y10	y	10	L
sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	494.253297	2	y9	y	9	E
sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	373.189968	2	y7	y	7	T
sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	225.613365	2	y4	y	4	S

sp Q5BJF6 ODFP2_HUMAN	WENPPHC[+57]LEITPPSSEK	1010.975289	2	0	182.097351	2	y3	y	3	S
sp Q5BJF6 ODFP2_HUMAN	QMTC[+57]TDINTLTR	727.342326	2	0	933.499986	1	y8	y	8	T
sp Q5BJF6 ODFP2_HUMAN	QMTC[+57]TDINTLTR	727.342326	2	0	490.298373	1	y4	y	4	T
sp Q5BJF6 ODFP2_HUMAN	QMTC[+57]TDINTLTR	727.342326	2	0	467.253631	2	y8	y	8	T
sp Q5BJF6 ODFP2_HUMAN	QMTC[+57]TDINTLTR	727.342326	2	0	416.729792	2	y7	y	7	D
sp Q5BJF6 ODFP2_HUMAN	QMTC[+57]TDINTLTR	727.342326	2	0	359.21632	2	y6	y	6	I
sp Q5BJF6 ODFP2_HUMAN	QMTC[+57]TDINTLTR	727.342326	2	0	245.652824	2	y4	y	4	T
sp Q5BJF6 ODFP2_HUMAN	QMTC[+57]TDINTLTR	727.342326	2	0	195.128985	2	y3	y	3	L
sp Q5BJF6 ODFP2_HUMAN	GHLQAQLR	461.7645	2	0	487.298707	1	y4	y	4	A
sp Q5BJF6 ODFP2_HUMAN	GHLQAQLR	461.7645	2	0	416.261593	1	y3	y	3	Q
sp Q5BJF6 ODFP2_HUMAN	GHLQAQLR	461.7645	2	0	244.152992	2	y4	y	4	A
sp Q5BJF6 ODFP2_HUMAN	GHLQAQLR	461.7645	2	0	208.634435	2	y3	y	3	Q
sp Q5BJF6 ODFP2_HUMAN	LNQAHLEVQQLK	710.898982	2	0	857.509094	1	y7	y	7	L
sp Q5BJF6 ODFP2_HUMAN	LNQAHLEVQQLK	710.898982	2	0	744.42503	1	y6	y	6	E
sp Q5BJF6 ODFP2_HUMAN	LNQAHLEVQQLK	710.898982	2	0	615.382437	1	y5	y	5	V
sp Q5BJF6 ODFP2_HUMAN	LNQAHLEVQQLK	710.898982	2	0	516.314023	1	y4	y	4	Q
sp Q5BJF6 ODFP2_HUMAN	LNQAHLEVQQLK	710.898982	2	0	497.787641	2	y8	y	8	H
sp Q5BJF6 ODFP2_HUMAN	LNQAHLEVQQLK	710.898982	2	0	308.194856	2	y5	y	5	V
sp Q5BJF6 ODFP2_HUMAN	LAEC[+57]QDQLQGYER	805.367386	2	0	1136.533077	1	y9	y	9	Q
sp Q5BJF6 ODFP2_HUMAN	LAEC[+57]QDQLQGYER	805.367386	2	0	1008.474499	1	y8	y	8	D
sp Q5BJF6 ODFP2_HUMAN	LAEC[+57]QDQLQGYER	805.367386	2	0	893.447556	1	y7	y	7	Q
sp Q5BJF6 ODFP2_HUMAN	LAEC[+57]QDQLQGYER	805.367386	2	0	652.304915	1	y5	y	5	Q
sp Q5BJF6 ODFP2_HUMAN	LAEC[+57]QDQLQGYER	805.367386	2	0	467.224873	1	y3	y	3	Y
sp Q5BJF6 ODFP2_HUMAN	LAEC[+57]QDQLQGYER	805.367386	2	0	262.626807	2	y4	y	4	G
sp Q5BJF6 ODFP2_HUMAN	EEAIHQSQLR	605.812376	2	0	768.411111	1	y6	y	6	H
sp Q5BJF6 ODFP2_HUMAN	EEAIHQSQLR	605.812376	2	0	503.293622	1	y4	y	4	S

sp Q5BJF6 ODFP2_HUMAN	EEAIHQSQLR	605.812376	2	0	416.261593	1	y3	y	3	Q
sp Q5BJF6 ODFP2_HUMAN	EEAIHQSQLR	605.812376	2	0	316.179738	2	y5	y	5	Q
sp Q5BJF6 ODFP2_HUMAN	EEAIHQSQLR	605.812376	2	0	252.150449	2	y4	y	4	S
sp Q5BJF6 ODFP2_HUMAN	EEAIHQSQLR	605.812376	2	0	208.634435	2	y3	y	3	Q
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	566.285659	2	0	674.34678	1	y6	y	6	A
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	566.285659	2	0	603.309666	1	y5	y	5	I
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	566.285659	2	0	490.225602	1	y4	y	4	E
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	566.285659	2	0	361.183009	1	y3	y	3	D
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	566.285659	2	0	302.158471	2	y5	y	5	I
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	566.285659	2	0	245.616439	2	y4	y	4	E
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	566.285659	2	0	181.095142	2	y3	y	3	D
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	797.455602	1	y6	y	6	Y
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	634.392273	1	y5	y	5	V
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	535.323859	1	y4	y	4	Q
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	407.265282	1	y3	y	3	F
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	399.231439	2	y6	y	6	Y
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	317.699775	2	y5	y	5	V
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	268.165568	2	y4	y	4	Q
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	629.318448	2	0	204.136279	2	y3	y	3	F
sp O43505 B4GA1_HUMAN	YEAAVPDPR	509.253631	2	0	583.319837	1	y5	y	5	V
sp O43505 B4GA1_HUMAN	YEAAVPDPR	509.253631	2	0	484.251423	1	y4	y	4	P
sp O43505 B4GA1_HUMAN	YEAAVPDPR	509.253631	2	0	387.198659	1	y3	y	3	D
sp O43505 B4GA1_HUMAN	YEAAVPDPR	509.253631	2	0	292.163556	2	y5	y	5	V
sp O43505 B4GA1_HUMAN	YEAAVPDPR	509.253631	2	0	242.629349	2	y4	y	4	P
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	1169.550701	1	y10	y	10	S
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	967.49173	1	y8	y	8	F

sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	634.359259	1	y5	y	5	C
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	474.32861	1	y4	y	4	L
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	628.795003	2	y11	y	11	S
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	585.278989	2	y10	y	10	S
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	541.762974	2	y9	y	9	D
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	484.249503	2	y8	y	8	F
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	410.715296	2	y7	y	7	D
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	353.201824	2	y6	y	6	A
sp P13987 CD59_HUMAN	TAVNC[+57]SSDFDAC[+57]LITK	901.408394	2	0	317.683267	2	y5	y	5	C
sp P13987 CD59_HUMAN	AGLQVYNK	446.747984	2	0	523.287474	1	y4	y	4	V
sp P13987 CD59_HUMAN	AGLQVYNK	446.747984	2	0	424.21906	1	y3	y	3	Y
sp P13987 CD59_HUMAN	AGLQVYNK	446.747984	2	0	262.147375	2	y4	y	4	V
sp P13987 CD59_HUMAN	AGLQVYNK	446.747984	2	0	212.613168	2	y3	y	3	Y
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	894.348436	1	y6	y	6	T
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	793.300758	1	y5	y	5	Y
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	630.237429	1	y4	y	4	Y
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	467.174101	1	y3	y	3	C
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	447.677856	2	y6	y	6	T
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	397.154017	2	y5	y	5	Y
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	315.622353	2	y4	y	4	Y
sp P13987 CD59_HUMAN	ENELTYYC[+57]C[+57]K	690.283945	2	0	234.090688	2	y3	y	3	C
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	1391.664879	1	y13	y	13	E
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	892.437051	1	y9	y	9	N
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	721.37266	1	y7	y	7	G
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	563.303518	1	y5	y	5	S
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	363.187425	1	y3	y	3	S

sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	696.336078	2	y13	y	13	E
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	446.722164	2	y9	y	9	N
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	389.7007	2	y8	y	8	G
sp P13987 CD59_HUMAN	DLC[+57]NFNEQLENGGTSLSEK	1077.98404	2	0	282.155397	2	y5	y	5	S
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	1059.460246	1	y9	y	9	G
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	1002.438783	1	y8	y	8	E
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	630.310669	1	y5	y	5	N
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	516.267741	1	y4	y	4	G
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	459.246278	1	y3	y	3	H
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	710.815647	2	y12	y	12	V
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	661.28144	2	y11	y	11	F
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	530.233761	2	y9	y	9	G
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	1045.44795	2	0	437.201733	2	y7	y	7	N
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	1074.532683	1	y10	y	10	E
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	945.49009	1	y9	y	9	T
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	844.442411	1	y8	y	8	H
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	707.383499	1	y7	y	7	G
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	579.324922	1	y5	y	5	G
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	522.303458	1	y4	y	4	F
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	619.301644	2	y11	y	11	Y
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	473.248683	2	y9	y	9	T
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	422.724844	2	y8	y	8	H
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	354.195388	2	y7	y	7	G
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	325.684656	2	y6	y	6	A
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	290.166099	2	y5	y	5	G
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	261.655367	2	y4	y	4	F

sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	843.399543	2	0	188.12116	2	y3	y	3	S
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	1151.595618	1	y11	y	11	G
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	850.452976	1	y8	y	8	D
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	482.283391	1	y4	y	4	H
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	345.22448	1	y3	y	3	I
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	576.301447	2	y11	y	11	G
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	368.216654	2	y7	y	7	V
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	318.682447	2	y6	y	6	G
sp O14786 NRP1_HUMAN	LEIWDGFDPDVGPHIGR	904.459935	2	0	290.171716	2	y5	y	5	P
sp O14786 NRP1_HUMAN	FVTAVGTQGAISK	639.856252	2	0	860.483607	1	y9	y	9	V
sp O14786 NRP1_HUMAN	FVTAVGTQGAISK	639.856252	2	0	475.287474	1	y5	y	5	G
sp O14786 NRP1_HUMAN	FVTAVGTQGAISK	639.856252	2	0	347.228896	1	y3	y	3	I
sp O14786 NRP1_HUMAN	FVTAVGTQGAISK	639.856252	2	0	430.745442	2	y9	y	9	V
sp O14786 NRP1_HUMAN	FVTAVGTQGAISK	639.856252	2	0	381.211235	2	y8	y	8	G
sp O14786 NRP1_HUMAN	IGYSNNGSDWK	620.783284	2	0	706.315479	1	y6	y	6	N
sp O14786 NRP1_HUMAN	IGYSNNGSDWK	620.783284	2	0	592.272552	1	y5	y	5	G
sp O14786 NRP1_HUMAN	IGYSNNGSDWK	620.783284	2	0	448.21906	1	y3	y	3	D
sp O14786 NRP1_HUMAN	IGYSNNGSDWK	620.783284	2	0	353.661378	2	y6	y	6	N
sp O14786 NRP1_HUMAN	IGYSNNGSDWK	620.783284	2	0	268.129182	2	y4	y	4	S
sp Q6UW49 SPESP_HUMAN	SVPSGEPGR	443.224873	2	0	699.342029	1	y7	y	7	P
sp Q6UW49 SPESP_HUMAN	SVPSGEPGR	443.224873	2	0	515.257236	1	y5	y	5	G
sp Q6UW49 SPESP_HUMAN	SVPSGEPGR	443.224873	2	0	329.193179	1	y3	y	3	P
sp Q6UW49 SPESP_HUMAN	SVPSGEPGR	443.224873	2	0	350.174652	2	y7	y	7	P
sp Q6UW49 SPESP_HUMAN	SVPSGEPGR	443.224873	2	0	258.132256	2	y5	y	5	G

sp Q6UW49 SPESP_HUMAN	SVPSGEPGR	443.224873	2	0	229.621524	2	y4	y	4	E
sp Q6UW49 SPESP_HUMAN	MLPVVTESTSPYVTSYK	994.997899	2	0	1219.584109	1	y11	y	11	S
sp Q6UW49 SPESP_HUMAN	MLPVVTESTSPYVTSYK	994.997899	2	0	1045.520053	1	y9	y	9	T
sp Q6UW49 SPESP_HUMAN	MLPVVTESTSPYVTSYK	994.997899	2	0	498.255839	1	y4	y	4	T
sp Q6UW49 SPESP_HUMAN	MLPVVTESTSPYVTSYK	994.997899	2	0	397.208161	1	y3	y	3	S
sp Q6UW49 SPESP_HUMAN	MLPVVTESTSPYVTSYK	994.997899	2	0	429.223811	2	y7	y	7	P
sp Q6UW49 SPESP_HUMAN	MLPVVTESTSPYVTSYK	994.997899	2	0	299.165765	2	y5	y	5	V
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	717.377745	1	y6	y	6	N
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	603.334818	1	y5	y	5	D
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	373.280932	1	y3	y	3	I
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	665.817324	2	y11	y	11	P
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	416.213974	2	y7	y	7	N
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	302.171047	2	y5	y	5	D
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	244.657575	2	y4	y	4	D
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	734.34678	2	0	187.144104	2	y3	y	3	I
sp Q6UW49 SPESP_HUMAN	LYEYLDIK	528.784233	2	0	488.307875	1	y4	y	4	L
sp Q6UW49 SPESP_HUMAN	LYEYLDIK	528.784233	2	0	375.223811	1	y3	y	3	D
sp Q6UW49 SPESP_HUMAN	LYEYLDIK	528.784233	2	0	244.657575	2	y4	y	4	L
sp Q6UW49 SPESP_HUMAN	LYEYLDIK	528.784233	2	0	188.115543	2	y3	y	3	D
sp Q6UW49 SPESP_HUMAN	AATVFNTLK	482.776742	2	0	622.355888	1	y5	y	5	F
sp Q6UW49 SPESP_HUMAN	AATVFNTLK	482.776742	2	0	475.287474	1	y4	y	4	N
sp Q6UW49 SPESP_HUMAN	AATVFNTLK	482.776742	2	0	361.244546	1	y3	y	3	T
sp Q6UW49 SPESP_HUMAN	AATVFNTLK	482.776742	2	0	311.681582	2	y5	y	5	F
sp Q6UW49 SPESP_HUMAN	AATVFNTLK	482.776742	2	0	238.147375	2	y4	y	4	N
sp Q6UW49 SPESP_HUMAN	AATVFNTLK	482.776742	2	0	181.125911	2	y3	y	3	T
sp P07602 SAP_HUMAN	GSAVWC[+57]QNVK	574.77949	2	0	834.392684	1	y6	y	6	W

sp P07602 SAP_HUMAN	GSAVWC[+57]QNVK	574.77949	2	0	648.313371	1	y5	y	5	C
sp P07602 SAP_HUMAN	GSAVWC[+57]QNVK	574.77949	2	0	488.282723	1	y4	y	4	Q
sp P07602 SAP_HUMAN	GSAVWC[+57]QNVK	574.77949	2	0	360.224145	1	y3	y	3	N
sp P07602 SAP_HUMAN	GSAVWC[+57]QNVK	574.77949	2	0	417.69998	2	y6	y	6	W
sp P07602 SAP_HUMAN	GSAVWC[+57]QNVK	574.77949	2	0	324.660324	2	y5	y	5	C
sp P07602 SAP_HUMAN	HC[+57]LQTVWNKPTVK	805.927217	2	0	971.567278	1	y8	y	8	V
sp P07602 SAP_HUMAN	HC[+57]LQTVWNKPTVK	805.927217	2	0	872.498864	1	y7	y	7	W
sp P07602 SAP_HUMAN	HC[+57]LQTVWNKPTVK	805.927217	2	0	686.419551	1	y6	y	6	N
sp P07602 SAP_HUMAN	HC[+57]LQTVWNKPTVK	805.927217	2	0	444.28166	1	y4	y	4	P
sp P07602 SAP_HUMAN	HC[+57]LQTVWNKPTVK	805.927217	2	0	347.228896	1	y3	y	3	T
sp P07602 SAP_HUMAN	HC[+57]LQTVWNKPTVK	805.927217	2	0	536.811116	2	y9	y	9	T
sp P07602 SAP_HUMAN	SLPC[+57]DIC[+57]K	496.73062	2	0	792.337872	1	y6	y	6	P
sp P07602 SAP_HUMAN	SLPC[+57]DIC[+57]K	496.73062	2	0	535.254459	1	y4	y	4	D
sp P07602 SAP_HUMAN	SLPC[+57]DIC[+57]K	496.73062	2	0	420.227516	1	y3	y	3	I
sp P07602 SAP_HUMAN	SLPC[+57]DIC[+57]K	496.73062	2	0	396.672574	2	y6	y	6	P
sp P07602 SAP_HUMAN	SLPC[+57]DIC[+57]K	496.73062	2	0	268.130868	2	y4	y	4	D
sp P07602 SAP_HUMAN	EIVDSYLPVILDIK	865.502946	2	0	1023.681245	1	y9	y	9	L
sp P07602 SAP_HUMAN	EIVDSYLPVILDIK	865.502946	2	0	910.597181	1	y8	y	8	P
sp P07602 SAP_HUMAN	EIVDSYLPVILDIK	865.502946	2	0	714.476003	1	y6	y	6	I
sp P07602 SAP_HUMAN	EIVDSYLPVILDIK	865.502946	2	0	601.391939	1	y5	y	5	L
sp P07602 SAP_HUMAN	EIVDSYLPVILDIK	865.502946	2	0	488.307875	1	y4	y	4	D
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	984.554664	1	y9	y	9	P
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	756.461415	1	y7	y	7	Q
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	628.402838	1	y6	y	6	T
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	527.355159	1	y5	y	5	L
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	414.271095	1	y4	y	4	V

sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	315.202681	1	y3	y	3	P
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	492.78097	2	y9	y	9	P
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	378.734346	2	y7	y	7	Q
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	314.705057	2	y6	y	6	T
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	264.181218	2	y5	y	5	L
sp P07602 SAP_HUMAN	EMPMQTLVPAK	622.822509	2	0	207.639186	2	y4	y	4	V
sp P07602 SAP_HUMAN	NVIPALELVEPIK	717.931959	2	0	1108.661238	1	y10	y	10	P
sp P07602 SAP_HUMAN	NVIPALELVEPIK	717.931959	2	0	940.57136	1	y8	y	8	L
sp P07602 SAP_HUMAN	NVIPALELVEPIK	717.931959	2	0	585.360639	1	y5	y	5	V
sp P07602 SAP_HUMAN	NVIPALELVEPIK	717.931959	2	0	486.292225	1	y4	y	4	E
sp P07602 SAP_HUMAN	NVIPALELVEPIK	717.931959	2	0	357.249632	1	y3	y	3	P
sp P07602 SAP_HUMAN	NVIPALELVEPIK	717.931959	2	0	554.834257	2	y10	y	10	P
sp P07602 SAP_HUMAN	SDVYC[+57]EVC[+57]EFLVK	824.373291	2	0	1183.548593	1	y9	y	9	C
sp P07602 SAP_HUMAN	SDVYC[+57]EVC[+57]EFLVK	824.373291	2	0	1023.517944	1	y8	y	8	E
sp P07602 SAP_HUMAN	SDVYC[+57]EVC[+57]EFLVK	824.373291	2	0	894.475351	1	y7	y	7	V
sp P07602 SAP_HUMAN	SDVYC[+57]EVC[+57]EFLVK	824.373291	2	0	795.406937	1	y6	y	6	C
sp P07602 SAP_HUMAN	SDVYC[+57]EVC[+57]EFLVK	824.373291	2	0	635.376289	1	y5	y	5	E
sp P07602 SAP_HUMAN	SDVYC[+57]EVC[+57]EFLVK	824.373291	2	0	506.333696	1	y4	y	4	F
sp P07602 SAP_HUMAN	SDVYC[+57]EVC[+57]EFLVK	824.373291	2	0	359.265282	1	y3	y	3	L
sp P07602 SAP_HUMAN	DGGFC[+57]EVC[+57]K	536.215334	2	0	695.285108	1	y5	y	5	C
sp P07602 SAP_HUMAN	DGGFC[+57]EVC[+57]K	536.215334	2	0	535.254459	1	y4	y	4	E
sp P07602 SAP_HUMAN	DGGFC[+57]EVC[+57]K	536.215334	2	0	348.146192	2	y5	y	5	C
sp P07602 SAP_HUMAN	DGGFC[+57]EVC[+57]K	536.215334	2	0	268.130868	2	y4	y	4	E
sp P07602 SAP_HUMAN	DGGFC[+57]EVC[+57]K	536.215334	2	0	203.609571	2	y3	y	3	V
sp P07602 SAP_HUMAN	GC[+57]SFLPDYQK	656.305538	2	0	860.451245	1	y7	y	7	L
sp P07602 SAP_HUMAN	GC[+57]SFLPDYQK	656.305538	2	0	747.367181	1	y6	y	6	P

sp P07602 SAP_HUMAN	GC[+57]SFLPDPYQK	656.305538	2	0	535.287474	1	y4	y	4	P
sp P07602 SAP_HUMAN	GC[+57]SFLPDPYQK	656.305538	2	0	430.72926	2	y7	y	7	L
sp P07602 SAP_HUMAN	GC[+57]SFLPDPYQK	656.305538	2	0	374.187228	2	y6	y	6	P
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	1114.544105	1	y9	y	9	Y
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	951.480776	1	y8	y	8	T
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	850.433098	1	y7	y	7	H
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	713.374186	1	y6	y	6	V
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	614.305772	1	y5	y	5	C
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	454.275124	1	y4	y	4	D
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	339.248181	1	y3	y	3	A
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	557.775691	2	y9	y	9	Y
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	476.244026	2	y8	y	8	T
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	425.720187	2	y7	y	7	H
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	357.190731	2	y6	y	6	V
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	307.656524	2	y5	y	5	C
peptides1	THC[+57]LYTHVC[+57]DAIK	813.386342	2	0	227.6412	2	y4	y	4	D

Table S9: Comparison analysis of Significant DEPs between Control and COVID-19 recovered

Protein	Peptide	Isotope Label Type	Fold Change Result	Log 2 Fold Change	P-Value	Adjusted P-Value
sp P04279 SEMG1_HUMAN	LPSEFSQFPHGQK	light	0.71 (95% CI:0.28 to 1.78)	-0.4922	0.450189206661492	0.6233
sp P04279 SEMG1_HUMAN	GSFSIQYTYHVDANDHDQSR	light	0.72 (95% CI:0.25 to 2.09)	-0.4698	0.533737035434571	0.6717
sp P04279 SEMG1_HUMAN	HLGGSQQLLHMK	light	0.3 (95% CI:0.08 to 1.11)	-1.7194	0.0704613942411025	0.2927
sp P04279 SEMG1_HUMAN	GISSQYSNTEER	light	0.65 (95% CI:0.35 to 1.22)	-0.6212	0.171845959417347	0.3839
sp P04279 SEMG1_HUMAN	EQTSVSGAQK	light	0.67 (95% CI:0.37 to 1.23)	-0.5694	0.190851392973141	0.3839
sp P04279 SEMG1_HUMAN	QGGSSQSSYVLQTEELVANK	light	0.52 (95% CI:0.2 to 1.35)	-0.9563	0.169795918319224	0.3839
sp P04279 SEMG1_HUMAN	GHYQNVVEVR	light	0.37 (95% CI:0.14 to 0.94)	-1.4505	0.0383883824318705	0.2927
sp P04279 SEMG1_HUMAN	VQTSLCPAHQDK	light	0.42 (95% CI:0.14 to 1.29)	-1.2462	0.124119097560214	0.3192
sp P04279 SEMG1_HUMAN	DIFSTQDELLVYNK	light	0.52 (95% CI:0.24 to 1.14)	-0.9355	0.098605363107092	0.3022
sp P04279 SEMG1_HUMAN	NLNQDQQHGR	light	0.46 (95% CI:0.14 to 1.56)	-1.1226	0.201841470210288	0.3839
sp P04279 SEMG1_HUMAN	QITIPSQEQEHSQK	light	0.44 (95% CI:0.18 to 1.06)	-1.1994	0.06668665147885	0.2927

sp P04279 SEMG1_HUMAN	SQIQAPNPK	light	0.54 (95% CI:0.28 to 1.06)	-0.8819	0.0717476168104176	0.2927
sp P04279 SEMG1_HUMAN	QEPWHGENAK	light	0.5 (95% CI:0.27 to 0.95)	-0.9876	0.0358150717822874	0.2927
sp P04279 SEMG1_HUMAN	EQDLLSHEQK	light	0.44 (95% CI:0.21 to 0.91)	-1.1803	0.027839649119237	0.2927
sp Q9BS86 ZBPB1_HUMAN	VPSSVGHVLR	light	0.91 (95% CI:0.48 to 1.74)	-0.1328	0.772109265366062	0.8481
sp Q9BS86 ZBPB1_HUMAN	IVGSTSFVVK	light	0.39 (95% CI:0.09 to 1.66)	-1.3686	0.192163009058044	0.3839
sp Q9BS86 ZBPB1_HUMAN	SPHVLCVTQQLR	light	0.58 (95% CI:0.2 to 1.67)	-0.7862	0.298746724147626	0.4740
sp Q9BS86 ZBPB1_HUMAN	NAELIDPSFQWYGPK	light	0.46 (95% CI:0.21 to 1.04)	-1.1079	0.0627172561014133	0.2927
sp Q9BS86 ZBPB1_HUMAN	LLLDLSCEISLLK	light	1.4 (95% CI:0.6 to 3.26)	0.4805	0.426937594162596	0.6136
sp Q9BS86 ZBPB1_HUMAN	CTDHNCEPYK	light	0.95 (95% CI:0.54 to 1.69)	-0.0704	0.862898258163536	0.8836
sp Q5BJF6 ODFP2_HUMAN	SSARPVGCK	light	0.94 (95% CI:0.41 to 2.12)	-0.0966	0.867229581914021	0.8836
sp Q5BJF6 ODFP2_HUMAN	WENPPHCLEITPPSSEK	light	0.46 (95% CI:0.14 to 1.48)	-1.1298	0.182736765505192	0.3839
sp Q5BJF6 ODFP2_HUMAN	QMTCTDINTLTR	light	0.37 (95% CI:0.15 to 0.89)	-1.4415	0.0286974095324453	0.2927
sp Q5BJF6 ODFP2_HUMAN	GHLQAQLR	light	0.47 (95% CI:0.21 to 1.09)	-1.0778	0.0776730260332583	0.2927
sp Q5BJF6 ODFP2_HUMAN	LNQAHLEVQQLK	light	0.88 (95% CI:0.42 to 1.85)	-0.1858	0.725410310874224	0.8161

sp Q5BJF6 ODFP2_HUMAN	LAECQDQLQGYER	light	0.54 (95% CI:0.16 to 1.82)	-0.8887	0.307224975457292	0.4740
sp Q5BJF6 ODFP2_HUMAN	EEAIHQSQLR	light	0.56 (95% CI:0.26 to 1.21)	-0.8327	0.132160161921144	0.3244
sp Q5BJF6 ODFP2_HUMAN	QLESAIEDAR	light	1.26 (95% CI:0.7 to 2.27)	0.3298	0.431792416991333	0.6136
sp Q5BJF6 ODFP2_HUMAN	SMQNYVQFLK	light	0.73 (95% CI:0.27 to 2.02)	-0.4451	0.535410537327534	0.6717
sp O43505 B4GA1_HUMAN	YEAAVPDPR	light	0.62 (95% CI:0.37 to 1.07)	-0.6799	0.0813186069933738	0.2927
sp P13987 CD59_HUMAN	TAVNCSSDFDACLTK	light	0.91 (95% CI:0.32 to 2.56)	-0.1435	0.845488495820093	0.8836
sp P13987 CD59_HUMAN	AGLQVYNK	light	1.03 (95% CI:0.5 to 2.11)	0.0459	0.927742819837216	0.9277
sp P13987 CD59_HUMAN	ENELTYYCCK	light	0.87 (95% CI:0.39 to 1.91)	-0.2049	0.714804298311162	0.8161
sp P13987 CD59_HUMAN	DLCNFNEQLENGGTSLSK	light	1.16 (95% CI:0.37 to 3.63)	0.2195	0.785293644190491	0.8481
sp O14786 NRP1_HUMAN	YDYVEVFDGENENGHFR	light	0.55 (95% CI:0.14 to 2.2)	-0.8669	0.381766548990699	0.5726
sp O14786 NRP1_HUMAN	FVSDYETHGAGFSIR	light	0.52 (95% CI:0.24 to 1.13)	-0.9469	0.0960890288103569	0.3022
sp O14786 NRP1_HUMAN	LEIWDGFPDVGPHGR	light	1.3 (95% CI:0.44 to 3.82)	0.3766	0.622350468860188	0.7306
sp O14786 NRP1_HUMAN	FVTAVGTQGAISK	light	0.8 (95% CI:0.36 to 1.79)	-0.3193	0.57483066332374	0.6898
sp O14786 NRP1_HUMAN	IGYSNNGSDWK	light	0.74 (95% CI:0.29 to 1.92)	-0.4334	0.520985941823227	0.6717

sp Q6UW49 SPESP_HUMAN	SVPSGEPGR	light	0.72 (95% CI:0.39 to 1.33)	-0.4827	0.274364081308853	0.4490
sp Q6UW49 SPESP_HUMAN	MLPVVTESSTSPYVTSYK	light	0.7 (95% CI:0.21 to 2.32)	-0.5098	0.547311083258157	0.6717
sp Q6UW49 SPESP_HUMAN	HPESWNNDDILK	light	0.54 (95% CI:0.25 to 1.14)	-0.9001	0.100724638352931	0.3022
sp Q6UW49 SPESP_HUMAN	LYEYLDIK	light	0.6 (95% CI:0.36 to 1.01)	-0.727	0.0561652420191505	0.2927
sp Q6UW49 SPESP_HUMAN	AATVFNTLK	light	0.63 (95% CI:0.28 to 1.43)	-0.6608	0.258080240546737	0.4490
sp P07602 SAP_HUMAN	GSAVWCQNVK	light	0.59 (95% CI:0.38 to 0.92)	-0.7686	0.0210849643435731	0.2927
sp P07602 SAP_HUMAN	HCLQTVWNKPTVK	light	0.71 (95% CI:0.38 to 1.32)	-0.4884	0.271146388775449	0.4490
sp P07602 SAP_HUMAN	SLPCDICK	light	0.58 (95% CI:0.24 to 1.41)	-0.7915	0.218337188487439	0.3930
sp P07602 SAP_HUMAN	EIVDSYLPVILDIK	light	0.48 (95% CI:0.19 to 1.23)	-1.0493	0.122266489938731	0.3192
sp P07602 SAP_HUMAN	EMPMQTLVPAK	light	0.57 (95% CI:0.27 to 1.18)	-0.8208	0.12250746656652	0.3192
sp P07602 SAP_HUMAN	NVIPALELVEPIK	light	0.5 (95% CI:0.25 to 1.01)	-1.0046	0.0520869252254208	0.2927
sp P07602 SAP_HUMAN	SDVYCEVCEFLVK	light	0.45 (95% CI:0.22 to 0.91)	-1.1436	0.0279738577567652	0.2927
sp P07602 SAP_HUMAN	DGGFCEVCK	light	0.5 (95% CI:0.24 to 1.01)	-1.0114	0.0531179584721049	0.2927
sp P07602 SAP_HUMAN	GCSFLPDYQK	light	0.71 (95% CI:0.26 to 1.92)	-0.4956	0.483857118064174	0.6532

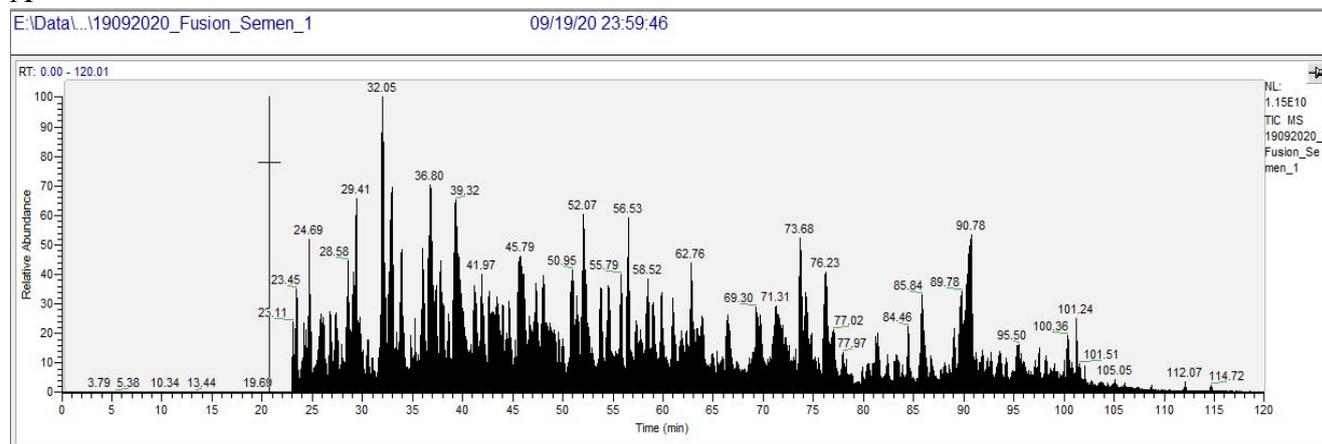
peptides1	THCLYTHVCDAIK	heavy	0.89 (95% CI:0.74 to 1.07)	-0.1717	0.206148621703603	0.3839
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ccc

Supplementary Figures

Figure S1

A



B

Thermo EASY-LC method print for Fusion

Sample pickup:

Volume [µl] : 3.00
Flow [µl / min] : 5.00

Sample loading:

Volume [µl] : 15.00
Flow [µl / min] : (unspecified)
Max. pressure [Bar] : 750.00

Gradient:

Time [mm:ss]	Duration [mm:ss]	Flow [nl/min]	Mixture [%B]
00:00	00:00	300.00	2.00
05:00	05:00	300.00	5.00
75:00	70:00	300.00	25.00
105:00	30:00	300.00	45.00
115:00	10:00	300.00	95.00
120:00	05:00	300.00	95.00

Pre-column equilibration:

Volume [µl] : 15.00
Flow [µl / min] : (unspecified)
Max. pressure [Bar] : 750.00

Analytical column equilibration:

Volume [µl] : 10.00
Flow [µl / min] : (unspecified)
Max. pressure [Bar] : 750.00

Autosampler wash:

Flush volume [µl] : 100.00

Orbitrap Fusion

Filter IntensityThreshold
Maximum Intensity = 1E+20
Minimum Intensity = 5000
Relative Intensity Threshold = 0
Intensity Filter Type = IntensityThreshold

Data Dependent Properties
Data Dependent Mode= Cycle Time
Scan Event 1

Scan ddMSnScan
MSn Level = 2
Isolation Mode = Quadrupole
Isolation Offset = Off
Isolation Window = 2
Reported Mass = Original Mass
Multi-notch Isolation = False
Scan Range Mode = Auto Normal
FirstMass = 100
Scan Priority= 1
ActivationType = HCD
Collision Energy Mode = Fixed
Collision Energy (%) = 30
Detector Type = Orbitrap
Orbitrap Resolution = 15K
Maximum Injection Time (ms) = 30
AGC Target = 10000
Inject ions for all available parallelizable time = True
Microscans = 1
Use ETD Internal Calibration = False
DataType = Centroid
Polarity = Positive
Source Fragmentation = False
Scan Description =

C

Orbitrap Fusion Method Summary

MININT-CVDF05E\Fusion

Global Settings

Use Ion Source Settings from Tune = True
Method Duration (min)= 120
Infusion Mode (LC)= False
FAIMS Mode = Not Installed
Internal Mass Calibration= User Defined Lock Mass
Application Mode = Peptide
Default Charge State = 1
Advanced Peak Determination = False
Xcalibur AcquireX enabled for method modifications = False
Internal Cal Positive
m/z
445.12003
Experiment 1
Experiment Name = MS
Start Time (min) = 0
End Time (min) = 120
Cycle Time (sec) = 3

Scan MasterScan

MSn Level = 1
Use Wide Quad Isolation = True
Detector Type = Orbitrap
Orbitrap Resolution = 500K
Mass Range = Normal
Scan Range (m/z) = 375-1700
Maximum Injection Time (ms) = 50
AGC Target = 400000
Microscans = 1
RF Lens (%) = 60
Use ETD Internal Calibration = False
DataType = Profile
Polarity = Positive
Source Fragmentation = False
Scan Description =

Filter MIPS

MIPS Mode = Peptide

Filter ChargeState

Include charge state(s) = 2-6
Include undetermined charge states = False
Include charge states 25 and higher = False

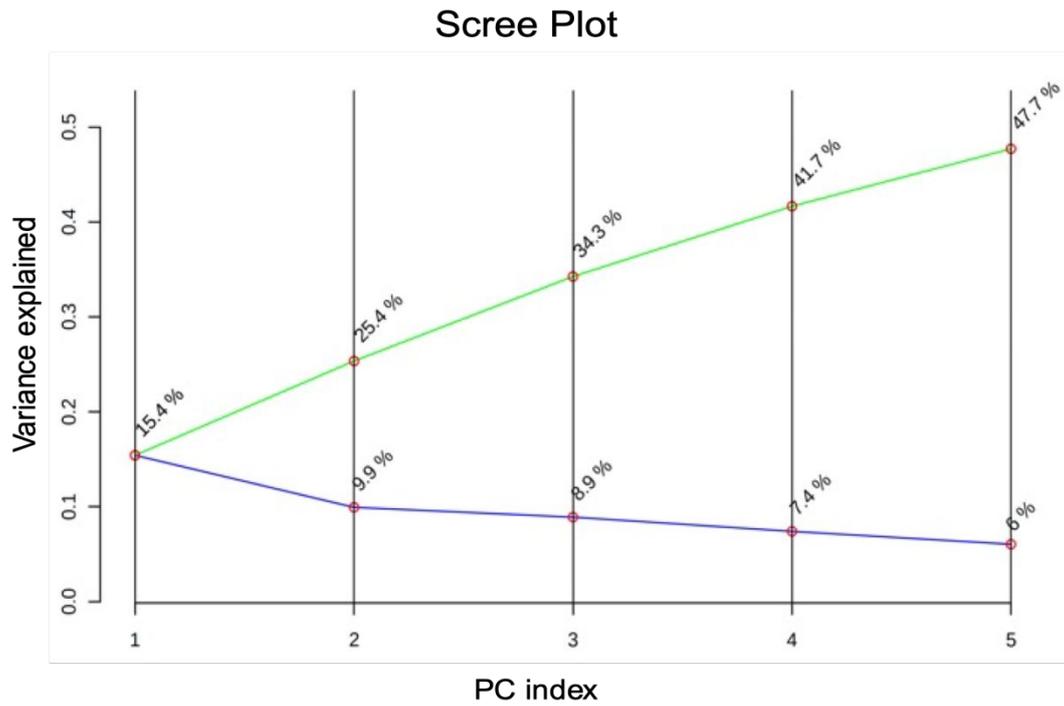
Filter DynamicExclusion

Exclude after n times = 1
Exclusion duration (s) = 40
Mass Tolerance = ppm
Mass tolerance low = 10
Mass tolerance high = 10
Exclude isotopes = True
Perform dependent scan on single charge state per precursor

Figure S1: Total ion chromatogram and MS settings used for the study. Figure 1A shows the representative TIC. It illustrates the summation of all ions obtained from each mass spectrometer scan at a given time. The relative abundance of all ions are plotted against time (min) as a function of time. The detailed nLC-MS parameters used for semen analysis are given in figure 1B and 1C.

Figure S2

A



B

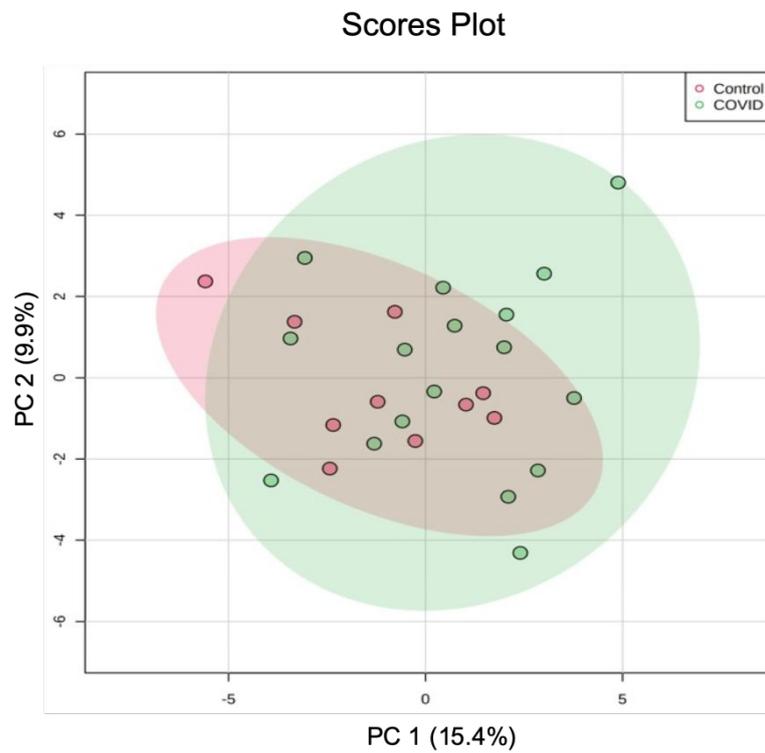
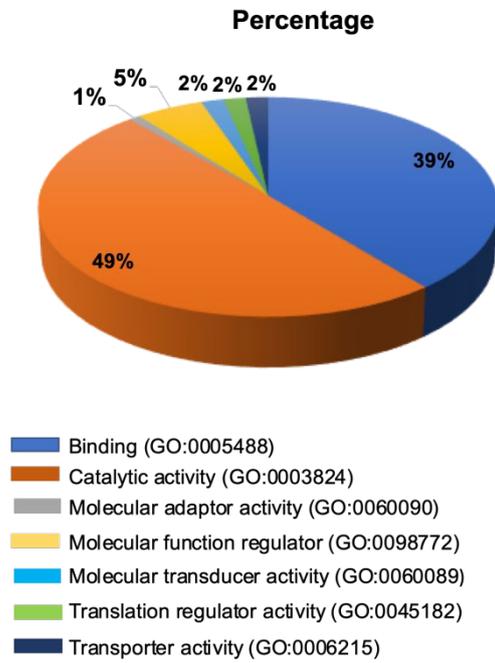


Figure S2: Principal Component Analysis of Control and COVID19-R (Recovered) patients. Figure 2A and 2B represent the variance over PC index plot and 2D plot of principal component based clustering of Control and COVID19-R.

Figure S3

A



B

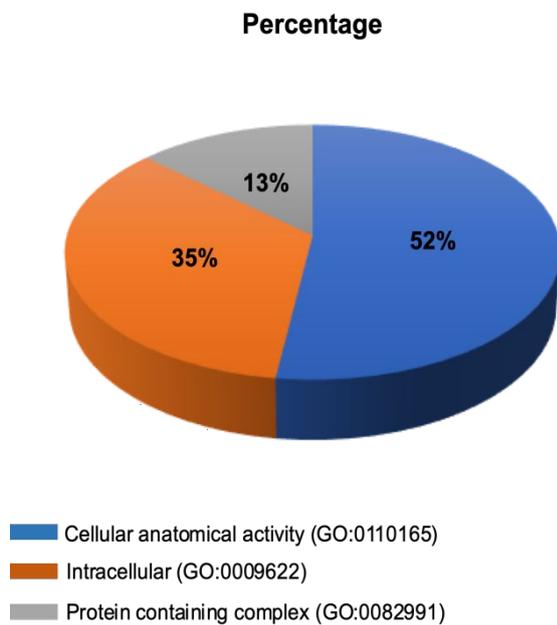
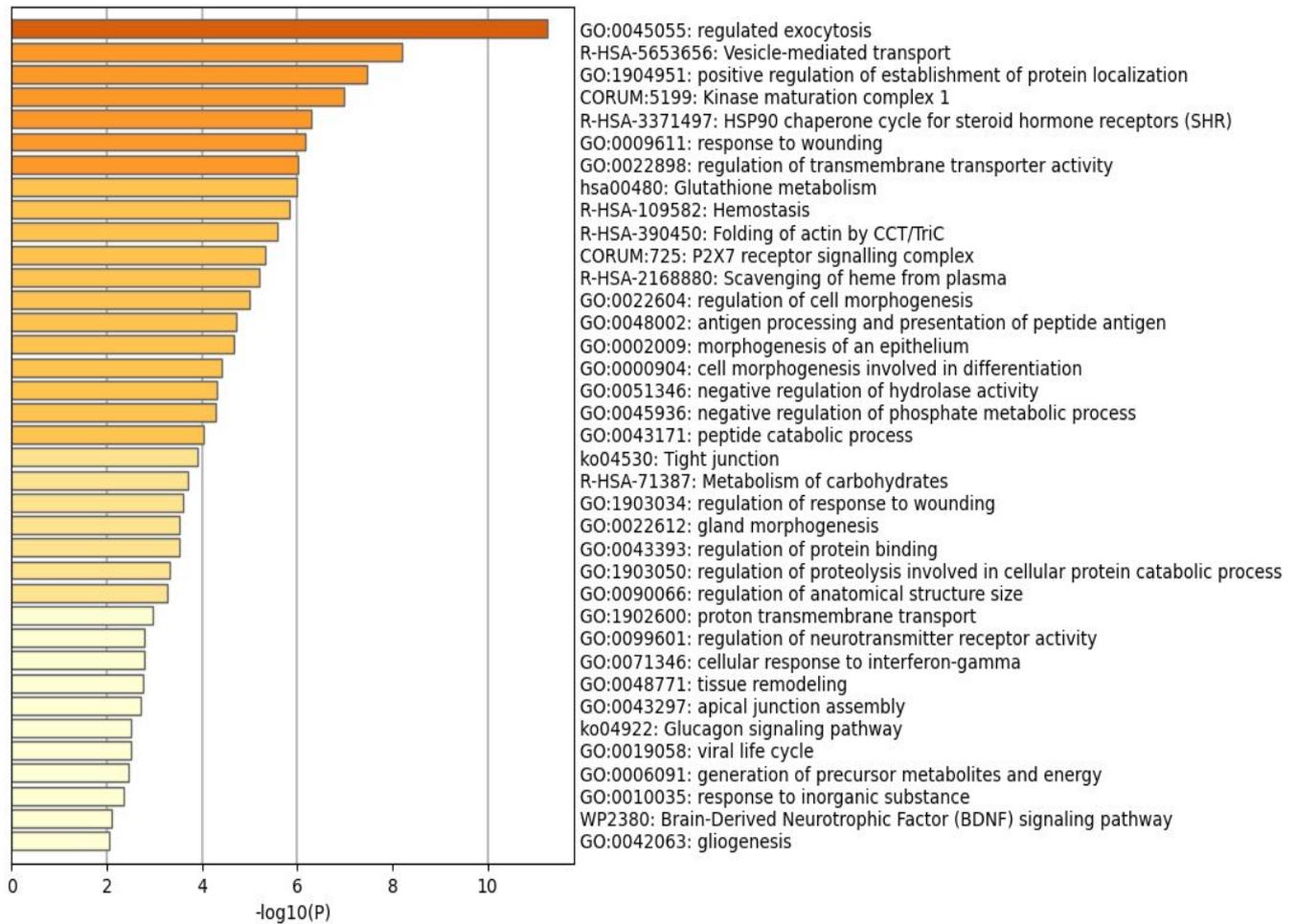


Figure S3: It shows the functional enriched term for major molecular function (3A) and cellular components for all the dysregulated proteins in COVID19-R (Recovered) vs. Control (3B).

Figure S4

A



B

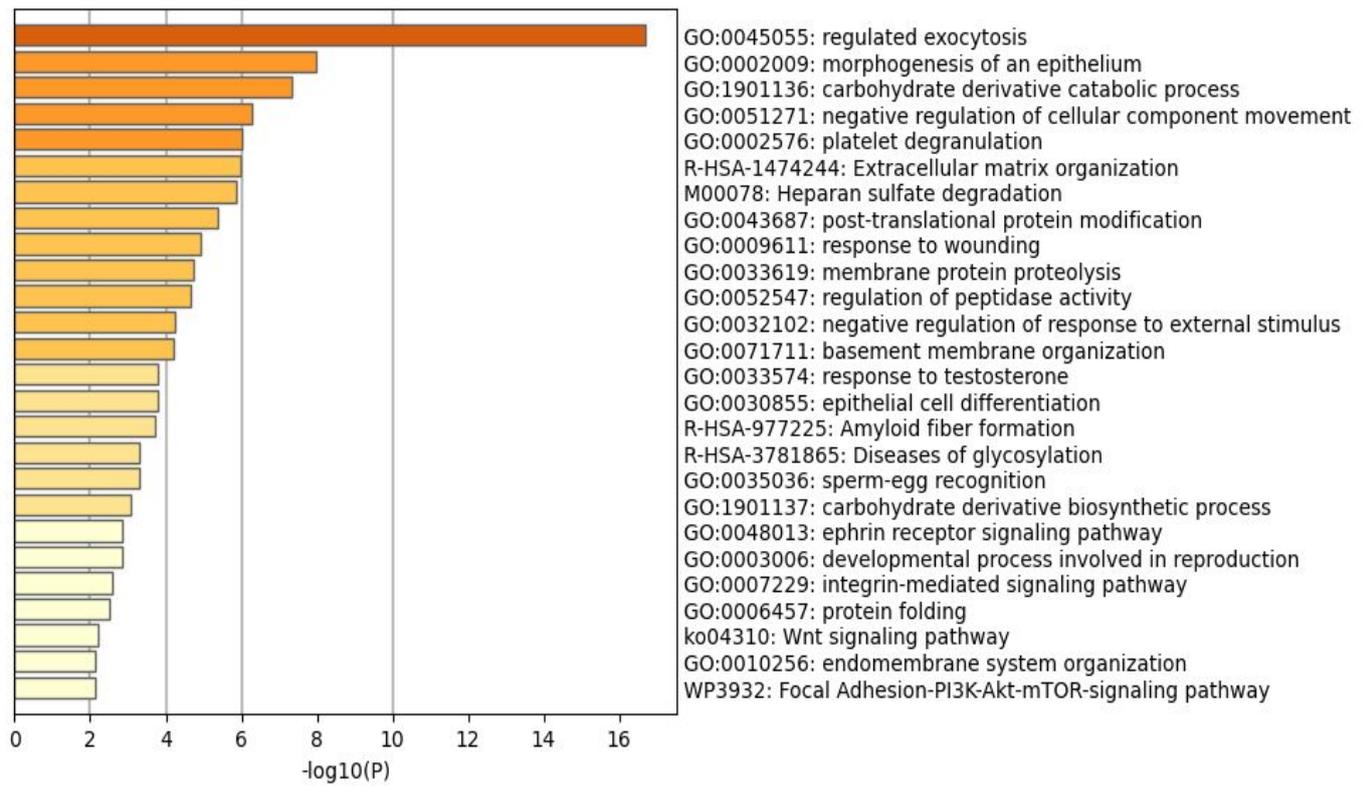


Figure S4: The bar graph shows the significant upregulated (4A) and downregulated pathways (4B) in COVID19-R (Recovered) patients as compared to control ($-\log_{10}P > 2$).

Figure S5

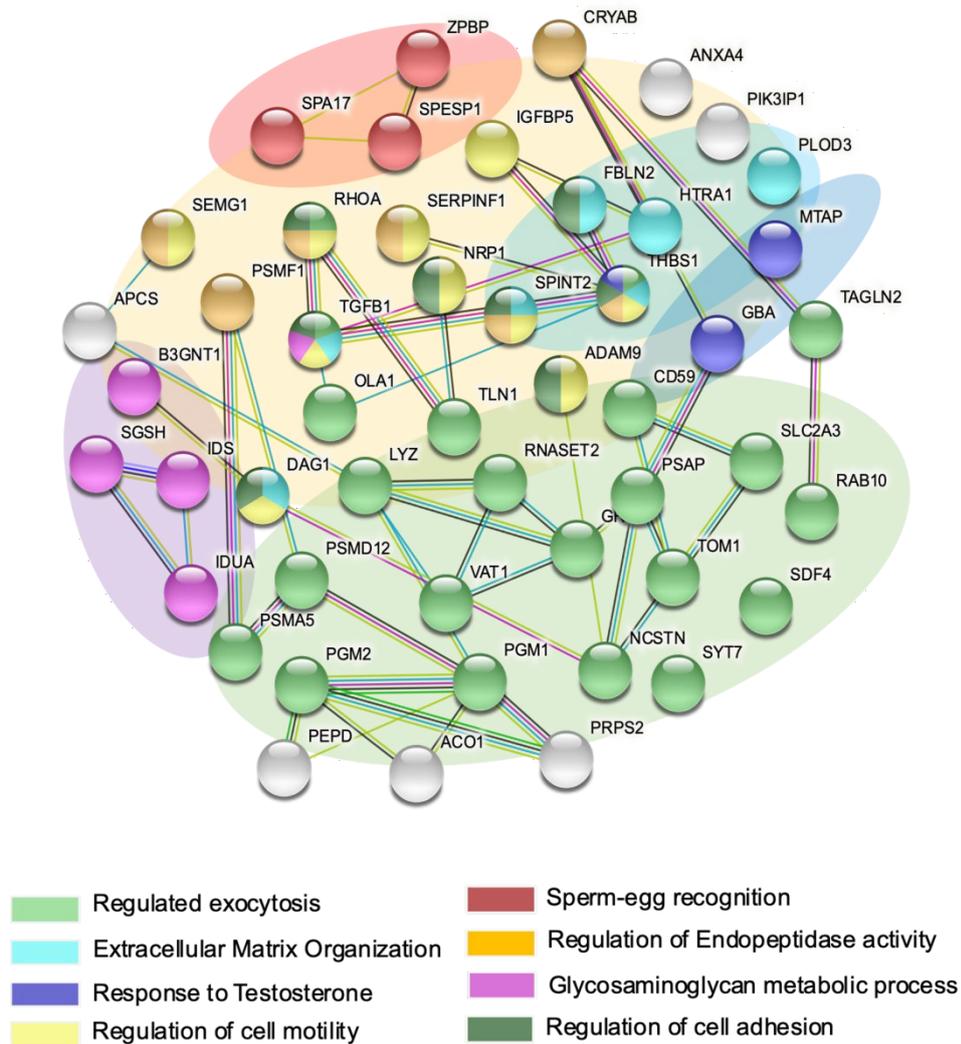
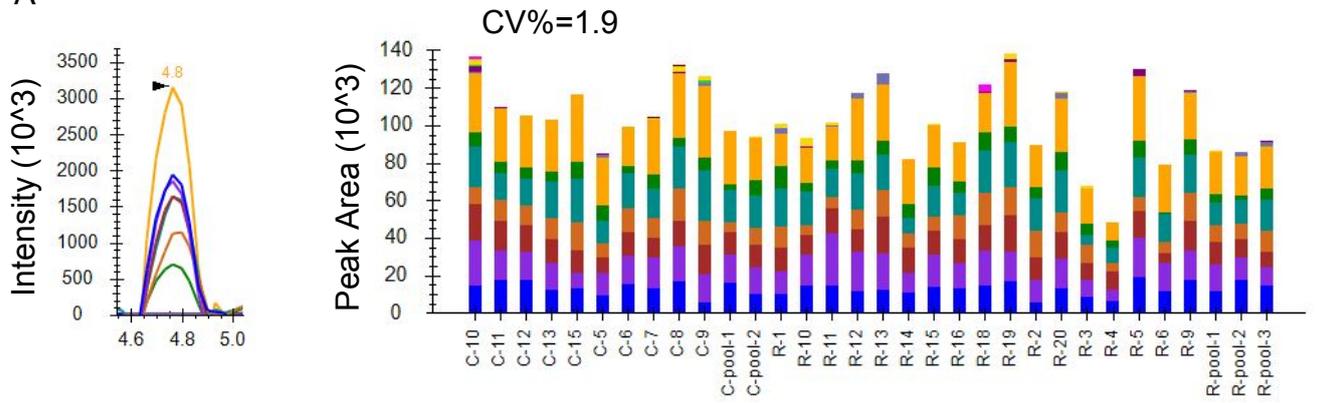


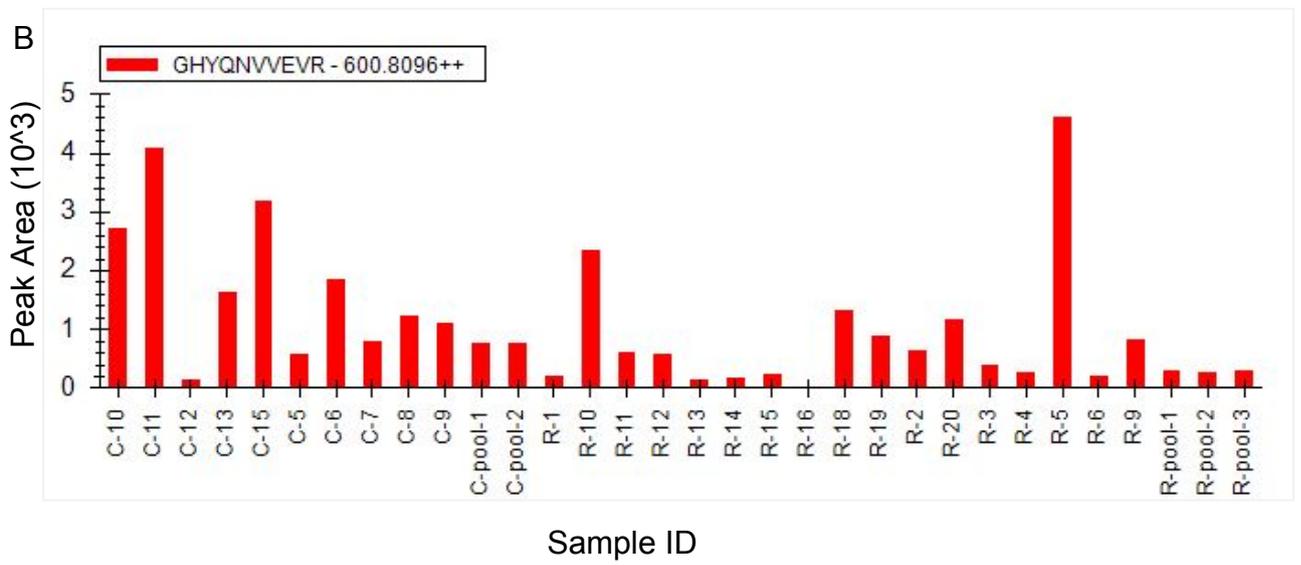
Figure S5: A protein-protein interaction network analysis of a few downregulated proteins associated with reproductive function. Regulated exocytosis (GO:0045055), Extracellular Matrix Organization (GO:0030198), Response to Testosterone (GO:0033574), Regulation of cell motility (GO:2000145), Sperm-egg recognition (GO:0035036), Regulation of Endopeptidase activity (GO:0052548), Glycosaminoglycan metabolic process (GO:0030203), Regulation of cell adhesion (GO:0030155)

Figure S6

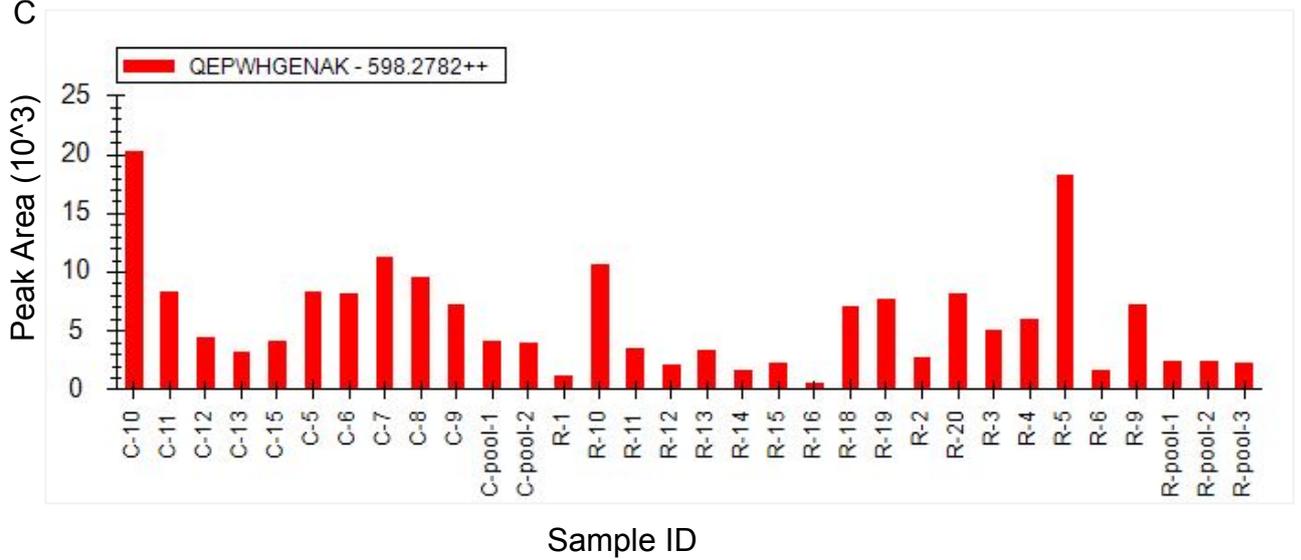
A



B



C



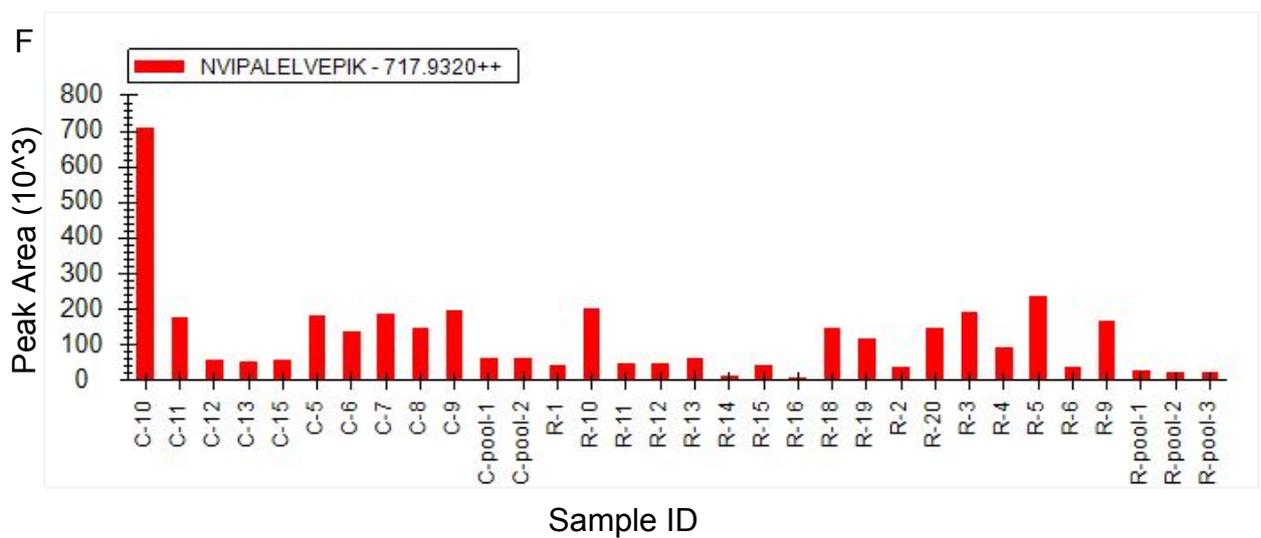
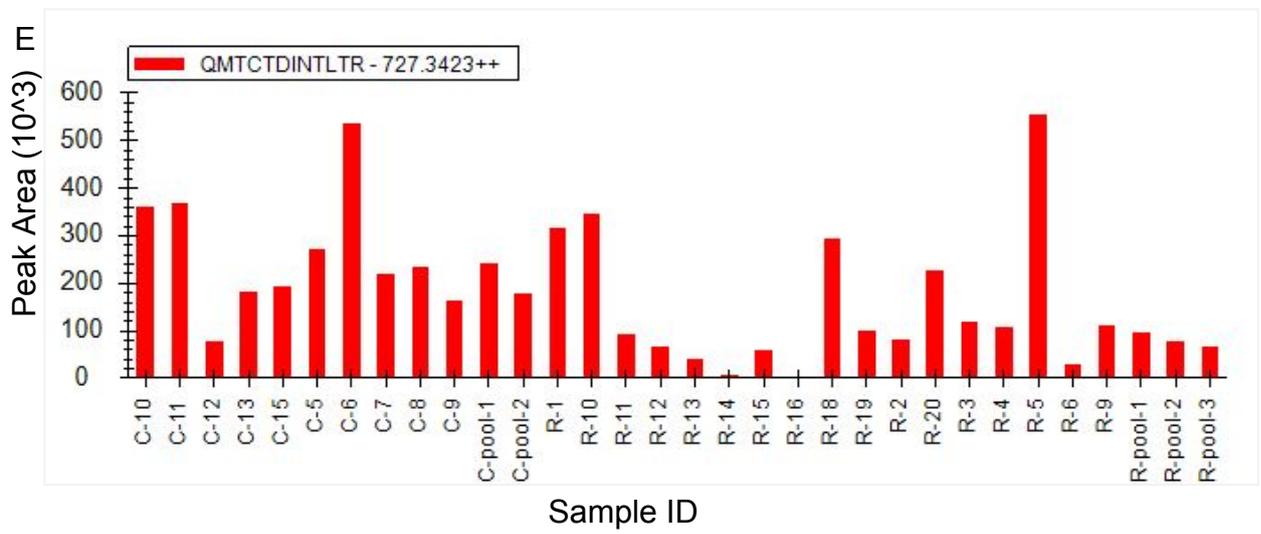
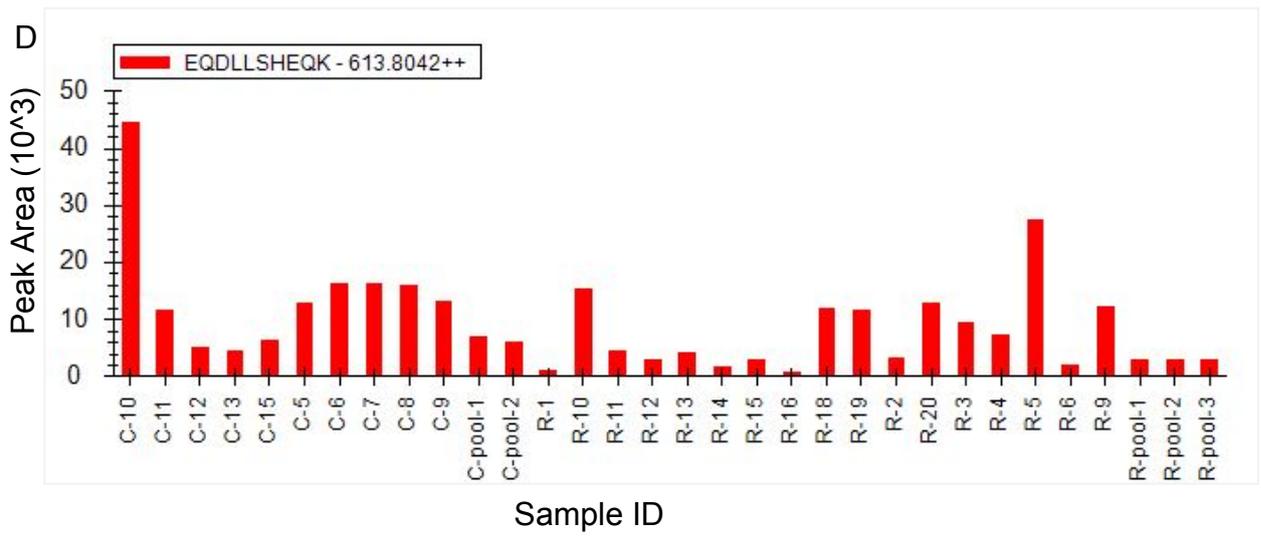


Figure S6: Comparative SRM intensity of significant peptides across the sample cohort. **6A** Representative peak for the spiked in heavy labelled synthetic peptide (THCLYTHVCDAIK) and its peak area across the sample cohort (C –Control, R- COVID19 recovered) showing a significant CV percentage value. **6B-6F** Bar plot showing the peak area for five significantly downregulated peptides (of SMG1, ODFP2 and SAP) across the samples.